

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:40:10 ; Search time 720.113 Seconds

```
Title: US-10-035-833A-7063
Perfect score: 41
Sequence: 1 tgtatcctgtgaagatcac.....gtatccttctctgcacatcg 41
```

Scoring table: IDENTITY\_NUC  
Gapo 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Database :

```

1:  gb_ba: *
2:  gb_htg: *
3:  gb_in: *
4:  gb_om: *
5:  gb_ov: *
6:  gb_pat: *
7:  gb_ph: *
8:  gb_pl: *
9:  gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40.6	99.0	41	6	AX515040	Sequence
2	40.6	99.0	41	6	AX520865	Sequence
3	40.6	99.0	79303	2	AC011074	Sequence
4	40.6	99.0	209156	2	AC009329	Sequence
5	40.6	99.0	211222	2	AC022097	Sequence
6	30	73.2	5735	6	AX348453	Sequence
7	25.2	61.5	85718	2	AC022660	Sequence
8	25.2	61.5	101941	2	AC010948	Sequence
9	25.2	61.5	142190	2	AC001415	Sequence
10	25.2	61.5	207743	2	AC048480	Sequence
11	24.6	60.0	5735	6	AX348452	Sequence
12	24.6	60.0	115525	9	AX348452	Sequence
13	24.6	59.5	110000	9	AX129465	Sequence
14	24.4	59.5	132200	2	AL161615	Sequence
15	24.4	59.5	141889	2	AC033006	Sequence
16	24.4	59.5	154055	2	AL157774	Sequence
17	24.4	59.5	176212	2	AC013326	Sequence
18	24.4	59.5	191592	2	AC118070	Sequence
19	24.4	59.5	214765	2	AC096238	Sequence

C	20	24	59.0	210789	2	AC124082
C	21	24	58.5	116214	8	AC113930
C	22	23.6	57.6	89723	8	AP001417
C	23	23.6	57.6	95518	5	BX568981
C	24	23.6	57.6	100000	9	AP000018
C	25	23.6	57.6	100000	9	AP000010
C	26	23.6	57.6	179881	10	AC121593
C	27	23.6	57.6	207747	9	BS000126
C	28	23.6	57.6	210040	10	AL133991
C	29	23.6	57.6	340000	9	AP001730
C	30	23.4	57.1	24432	1	MBP20MCH
C	31	23.4	57.1	2432	1	SL1233
C	32	23.4	57.1	11565	1	AE000874
C	33	23.4	57.1	194827	10	AC116583
C	34	23.4	57.1	216749	5	AL953893
C	35	23.4	57.1	216749	5	AC122042
C	36	23	56.1	274214	2	Mus muscu
C	37	23	56.1	430	9	H5233VYAS
C	38	23	56.1	72477	9	AC026111
C	39	23	56.1	193847	10	AC139757
C	40	23	56.1	196933	10	AC064793
C	41	23	56.1	233537	2	AC106105
C	42	23	56.1	233905	2	AC120465
C	43	23	56.1	256791	10	AC113961
C	44	23	56.1	261951	2	AC113869
C	45	22.8	55.6	110467	2	BX546490
C	46	22.8	55.6	135594	8	AC087220
C	47	22.8	55.6	147130	8	AC084765
C	48	22.8	55.6	224591	10	AC131710
C	49	22.8	55.6	244068	2	AC131345
C	50	22.8	55.6	245757	10	AC098788
C	51	22.8	55.6	245892	2	AC096984
C	52	22.8	55.6	253410	2	AC109250
C	53	22.6	55.6	257333	2	AC123722
C	54	22.6	55.1	179094	5	BX510934
C	55	22.6	55.1	190784	2	AC133669
C	56	22.6	55.1	222562	2	AC133851
C	57	22.6	55.1	237865	2	AC137843
C	58	22.6	55.1	255296	2	AC108538
C	59	22.6	55.1	324594	2	BX649342
C	60	22.6	55.1	332036	2	AC129629
C	61	22.4	54.6	160069	2	AC054867
C	62	22.4	54.6	165212	2	AC050762
C	63	22.4	54.6	172016	10	AC128671
C	64	22.4	54.6	176728	2	AC141032
C	65	22.4	54.6	181408	2	AC101891
C	66	22.4	54.6	181637	2	AC117451
C	67	22.4	54.6	198693	10	AL672150
C	68	22.4	54.6	201324	2	AC149607
C	69	22.4	54.6	204302	2	AC150700
C	70	22.4	54.6	204711	10	AC121884
C	71	22.4	54.6	215601	2	AC073806
C	72	22.4	54.6	223121	2	AC073726
C	73	22.4	54.6	251052	2	AC130129
C	74	22.4	54.6	263701	2	AC094442
C	75	22.2	54.1	12117	4	BT025687
C	76	22.2	54.1	100948	9	AL137012
C	77	22.2	54.1	108131	9	AL162427
C	78	22.2	54.1	110000	2	LMF1CHR1.12
C	79	22.2	54.1	150029	10	BX890639
C	80	22.2	54.1	163999	2	AC027143
C	81	22.2	54.1	175558	9	AL158823
C	82	22.2	54.1	186428	9	AC016355
C	83	22.2	54.1	195970	2	AC139216
C	84	22.2	54.1	197599	2	AC119769
C	85	22.2	54.1	218578	2	AL135978
C	86	22.2	54.1	220606	2	AC125958
C	87	22.2	54.1	232821	2	AC130860
C	88	22	53.7	400	11	GI6457
C	89	22	53.7	1068	8	AK068996
C	90	22	53.7	41378	8	AC005381
C	91	22	53.7	65332	8	AP004938
C	92	22	53.7	84581	9	AC024546
C	93	22	53.7	92775	9	AL441964
C	94	22	53.7	92775	9	AL441964
C	95	22	53.7	92775	9	AL441964
C	96	22	53.7	92775	9	AL441964
C	97	22	53.7	92775	9	AL441964
C	98	22	53.7	92775	9	AL441964
C	99	22	53.7	92775	9	AL441964
C	100	22	53.7	92775	9	AL441964

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:11:10 ; Search time 1452.89 Seconds

(without alignments)  
1028.317 Million cell updates/sec

Title: US-10-035-833a-7074

Perfect score: 41  
Sequence: 1 tctcataggtcaaaaaaa.....gtccacaaatagtgtgaat 41

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

Database :  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hnc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	339	2	BE925815 QV0-BN04
2	41	100.0	493	6	CA93356 cs3h08.y
3	41	100.0	580	7	W02900 za04h02.r1
4	40	97.6	585	1	A1536104 xue.p9.F9
5	39.4	96.1	663	5	B0686928 UI-cr-PD1
6	28.4	69.3	958	5	BQ723128 AGENCOURT
7	26.6	64.9	700	8	BH967938 cdg80905.
8	25.8	62.9	406	8	A2139688 SP_0001_A
9	25.4	62.0	666	9	BX337182 Danilo rer
10	25.2	61.5	765	8	BH524372 BOHRD37TR
11	25.2	61.5	793	8	BH467978 BOHRD50TR
12	25.2	61.5	793	8	BH579888 BB579888
13	25	61.0	470	8	AQ981773 RPT-23-3
14	25	61.0	684	8	A2615710 IM0445L01
15	25	61.0	749	9	CE636254 tigr-gss-
16	25	61.0	844	9	CR052915 Reverse s
17	25	61.0	844	9	CR052915 Reverse s
18	24.8	60.5	658	8	CC061138 MUQO.CH25
19	24.6	60.0	658	8	BH661890 BOMT149TF
20	24.6	60.0	666	8	BZ030044 oeg01e08.
21	24.6	60.0	672	9	AG163984 Pan_trcgl
22	24.6	60.0	709	9	CL148048 104_327_1
23	24.6	60.0	719	9	CL148047 104_327_1
24	24.6	60.0	743	8	AZ902924 RPT-24-1

C 25	24.4	59.5	612	2	BE436165	BE436165	EST407243
C 26	24.4	59.5	706	9	CE634961	CE634961	tigr-gss-
C 27	24.2	59.0	225	2	AW999474	MRO-BN07	AW999474
C 28	24.2	59.0	308	2	BB605325	BB605325	BB605325
C 29	24.2	59.0	342	2	AM296976	UI-H-BW0	AM296976
C 30	24.2	59.0	368	8	AO020044	CIT-HSP-2	AO020044
C 31	24.2	59.0	397	2	BE845728	232923.BA	BE845728
C 32	24.2	59.0	410	1	A1246601	pt65d08.x	A1246601
C 33	24.2	59.0	565	4	Bj086548	Bj086548	Bj086548
C 34	24.2	59.0	613	2	BF890898	PM2-MT010	BF890898
C 35	24.2	59.0	639	5	BP147813	BP147813	BP147813
C 36	24.2	59.0	640	8	BB663865	BB663865	BB663865
C 37	24.2	59.0	688	8	BZ014247	ce158902	BZ014247
C 38	24.2	59.0	856	4	BG843226	1024002A0	BG843226
C 39	24.2	59.0	2740	3	AK086969	Mus muscu	AK086969
C 40	24	58.5	200	2	BF170224	PCL0455.M	BF170224
C 41	24	58.5	265	1	A1058636	UI-R-Cl-X	A1058636
C 42	24	58.5	298	2	BF457396	UI-M-B21	BF457396
C 43	24	58.5	308	2	CG430266	ZMMBB025	CG430266
C 44	24	58.5	310	2	AM805973	CY1-JM010	AM805973
C 45	24	58.5	313	5	BQ195494	UI-R-CN1	BQ195494
C 46	24	58.5	392	2	AW693080	NF060A035	AW693080
C 47	24	58.5	422	2	AW136099	UI-H-B11	AW136099
C 48	24	58.5	479	7	H50650	yp66c02.s1	H50650
C 49	24	58.5	499	5	EX083094	EX083094	EX083094
C 50	24	58.5	512	9	CG706909	BARC.BFGL	CG706909
C 51	24	58.5	570	8	AZ254746	1165-T01	AZ254746
C 52	24	58.5	570	8	AZ903150	RPT-24-1	AZ903150
C 53	24	58.5	594	5	BUS51077	GM8800068	BUS51077
C 54	24	58.5	603	2	AM044394	xu10f09.x	AM044394
C 55	24	58.5	623	9	CG035936	PWM111TB	CG035936
C 56	24	58.5	629	6	CD402926	Gm_CK2553	CD402926
C 57	24	58.5	637	8	AO327166	nbxb0040D	AO327166
C 58	24	58.5	659	5	BK645610	DKFZ781D	BK645610
C 59	24	58.5	664	8	BZ953572	CH240-126	BZ953572
C 60	24	58.5	703	8	BZ509079	BONP187TR	BZ509079
C 61	24	58.5	714	8	BH257332	CH230-243	BH257332
C 62	24	58.5	720	8	BH280808	CH230-97E	BH280808
C 63	24	58.5	724	9	CC505950	CH240_347	CC505950
C 64	24	58.5	734	9	AC372289	Mus_muscu	AC372289
C 65	24	58.5	740	8	BH537638	BOGV886TR	BH537638
C 66	24	58.5	829	2	BF694440	602061617	BF694440
C 67	24	58.5	1041	9	CL493103	SAIL_574	CL493103
C 68	24	58.5	1290	9	CL643646	CH213-53H	CL643646
C 69	24	58.0	149	9	CR497547	Medicago	CR497547
C 70	23.8	58.0	324	1	A1454568	UI-R-BT0	A1454568
C 71	23.8	58.0	526	7	CN755384	ID0AA15C	CN755384
C 72	23.8	58.0	563	7	CO470143	SGP170073	CO470143
C 73	23.8	58.0	884	5	BU169441	TEICODON	BU169441
C 74	23.8	58.0	950	4	CNS0202V	Teicodon	CNS0202V
C 75	23.8	58.0	1162	8	CC277169	CH261-22G	CC277169
C 76	23.6	57.6	262	1	AV360132	AV360132	AV360132
C 77	23.6	57.6	308	2	AM155792	13447.MAR	AM155792
C 78	23.6	57.6	322	9	CE074585	tigr-gss-	CE074585
C 79	23.6	57.6	440	4	BG511638	saad07906	BG511638
C 80	23.6	57.6	452	8	BZ886509	CH240-126	BZ886509
C 81	23.6	57.6	526	4	BW882454	FB01053.Y	BW882454
C 82	23.6	57.6	534	8	BZ760022	622_UJ2_C	BZ760022
C 83	23.6	57.6	544	9	CR294587	Medicago	CR294587
C 84	23.6	57.6	700	8	CC069234	CSU-K33x.	CC069234
C 85	23.6	57.6	763	8	AO412002	CPG0952B	AO412002
C 86	23.6	57.6	801	7	CN650171	v6_p3_c20	CN650171
C 87	23.6	57.6	832	8	BZ209207	CH230-379	BZ209207
C 88	23.6	57.6	886	8	AZ202373	SP_0057_A	AZ202373
C 89	23.6	57.6	894	9	CC493317	CH240_327	CC493317
C 90	23.6	57.6	960	5	BU913485	AGENCOURT	BU913485
C 91	23.6	57.6	1201	8	CC222660	CH261-40A	CC222660
C 92	23.6	57.1	240	8	CE213483	tigr-gss-	CE213483
C 93	23.4	57.1	242	5	BO853432	BO853432	BO853432
C 94	23.4	57.1	249	9	BO849036	OGA9501.Y	BO849036
C 95	23.4	57.1	276	5	BO849036	OGA817.Y	BO849036
C 96	23.4	57.1	317	5	BO858034	OGB9C16.Y	BO858034
C 97	23.4	57.1	328	5	BO984287	OGB21E10.	BO984287

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OK nucleic - nucleic search, using sw model

Run on: October 31, 2004, 09:56:20 : Search time 158.775 Seconds  
[without alignments]  
1324.090 Million cell updates/sec

Title: US-10-035-833A-7074

Perfect score: 41

Sequence: 1 tctcacaagtgtaaaaaaa.....gtcacaatagtgtaaat 41

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA: \*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/PC1\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PC1US\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US10G\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	41	16	US-10-035-833A-7074
2	41	100.0	533	13	US-10-027-632-245152
3	41	100.0	533	13	US-10-027-632-245153
4	41	100.0	533	15	US-10-027-632-245152
5	41	100.0	533	15	US-10-027-632-245153
6	41	100.0	2181	10	US-09-999-686-10
7	41	100.0	2721	10	US-09-999-686-12
8	41	100.0	3118	10	US-09-999-686-19
9	41	100.0	3785	9	US-09-925-302-44
10	41	100.0	3785	10	US-09-925-302-44
11	41	100.0	5102	9	US-09-919-497-8
12	41	100.0	5102	9	US-09-954-531-153

13	41	100.0	5102	10	US-09-960-706-938	Sequence 938, App
14	41	100.0	5102	10	US-09-873-319-615	Sequence 615, App
15	41	100.0	5102	15	US-10-204-752-36	Sequence 36, Appl
16	41	100.0	5102	15	US-10-641-643-1426	Sequence 1426, Ap
17	41	100.0	5102	17	US-10-775-169-230	Sequence 230, App
18	41	100.0	5128	15	US-10-177-293-75	Sequence 95, Appl
19	41	100.0	5128	15	US-10-170-385-138	Sequence 138, App
20	41	100.0	5128	15	US-10-170-385-326	Sequence 326, App
21	41	100.0	5128	15	US-10-172-118-433	Sequence 433, App
22	41	100.0	5128	16	US-10-342-887-433	Sequence 433, App
23	41	100.0	5134	16	US-09-999-666-157	Sequence 1, Appl
24	41	100.0	5329	15	US-10-240-965-157	Sequence 157, App
25	29.8	72.7	630	14	US-10-198-846-790	Sequence 790, App
26	26.6	64.9	5371	16	US-10-221-714A-525	Sequence 525, App
27	25.6	62.4	700	13	US-10-027-632-25532	Sequence 25532, A
28	62.4	700	13	US-10-027-632-25532	Sequence 25532, A	
29	60.0	60968	15	US-10-085-117-181	Sequence 181, App	
30	59.0	71551.7	13	US-10-027-632-53712	Sequence 53712, A	
31	59.0	71551.7	13	US-10-027-632-53712	Sequence 53712, A	
32	58.5	50781	13	US-10-087-192-769	Sequence 769, App	
33	58.5	335913	10	US-09-754-853A-2	Sequence 2, Appl	
34	58.5	335913	10	US-09-754-853A-3	Sequence 3, Appl	
35	58.0	2050	14	US-10-097-065-58	Sequence 58, Appl	
36	58.0	2050	14	US-10-372-876-58	Sequence 58, Appl	
37	57.6	440	16	US-10-424-559-42431	Sequence 42431, A	
38	57.6	440	16	US-10-424-559-42431	Sequence 42431, A	
39	56.6	371	16	US-10-085-783A-29134	Sequence 29134, A	
40	56.6	371	16	US-10-085-783A-29134	Sequence 29134, A	
41	56.6	490	13	US-10-027-632-204329	Sequence 204329, A	
42	56.6	490	13	US-10-027-632-204329	Sequence 204329, A	
43	56.6	207433	16	US-10-126-022-5	Sequence 5, Appl	
44	56.6	207433	16	US-10-126-022-5	Sequence 5, Appl	
45	56.1	152	16	US-10-242-555A-29614	Sequence 29614, A	
46	56.1	152	16	US-10-085-783A-29614	Sequence 29614, A	
47	56.1	132	16	US-10-242-555A-29614	Sequence 29614, A	
48	56.1	432	16	US-10-085-783A-26442	Sequence 26442, A	
49	56.1	432	16	US-10-085-783A-26442	Sequence 26442, A	
50	56.1	458	13	US-10-027-632-57229	Sequence 57229, A	
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82	56.1	458	15	US-10-027-632-57229	Sequence 57229, A	
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:13:20 : Search time 37.1814 Seconds  
(without alignments)  
783.789 Million cell updates/sec

Title: US-10-035-833A-7074

Perfect score: 41  
Sequence: 1 tcccatagtgtaaaaaa.....gtccacaatagtgtaaat 41

Scoring table:

IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	41	100.0	5102	4	US-09-919-497-8
3	22.6	55.1	930	4	US-09-220-132-89
4	22.4	54.6	273	4	US-09-621-976-11078
5	22.4	54.6	1486	1	US-08-250-859-1
6	22.4	54.6	1486	1	US-08-347-029-1
7	22.4	54.6	1486	1	US-08-490-803-1
8	22.4	54.6	1486	2	US-08-457-254-1
9	22.4	54.6	1486	2	US-08-484-257-1
10	22.4	54.6	1486	3	US-08-999-927-3
11	22.4	54.6	1486	3	US-08-461-819-3
12	22.4	54.6	1486	5	PCT-US94-08806-1
13	22.4	54.6	1486	5	PCT-US95-01775-1
14	22.4	54.6	1486	5	PCT-US95-01829-3
15	22.4	54.6	1486	5	PCT-US95-14932-1
16	22.4	54.6	1486	5	PCT-US95-16626-1
17	22.2	54.1	168575	4	US-09-426-290-1
18	22	53.7	480	4	US-09-270-767-30573
19	22	53.7	572	4	US-09-270-767-14411
20	21.8	52.7	2621	4	US-09-673-335A-22
21	21.6	52.7	540	4	US-09-248-796A-6021
22	21.4	52.2	1863	4	US-09-248-796A-2811
23	21.4	52.2	99629	4	US-09-596-002-37
24	21.2	51.7	6400	4	US-09-976-594-61
25	21	51.2	193	4	US-09-513-999C-24677
26	21	51.2	265	4	US-09-513-999C-36085
27	21	51.2	970	3	US-08-791-115B-16

28	21	51.2	970	4	US-09-140-749-27	Sequence 27, Appl
29	21	51.2	3680	4	US-09-647-390-15	Sequence 15, Appl
30	21	51.2	4084	2	US-08-568-459A-1	Sequence 1, Appl
31	21	51.2	4084	2	US-08-487-826B-1	Sequence 1, Appl
32	21	51.2	4084	3	US-09-210-288-1	Sequence 1, Appl
33	21	51.2	4084	6	5198347-5	Patent No. 5198347
34	20.8	50.7	419	4	US-09-513-999C-31472	Sequence 31, Appl
35	20.8	50.7	471	4	US-09-270-767-5979	Sequence 5979, Ap
36	20.8	50.7	471	4	US-09-270-767-11261	Sequence 11261, A
37	20.8	50.7	599	4	US-09-270-767-12759	Sequence 12759, A
38	20.8	50.7	1419	4	US-09-270-767-30657	Sequence 30657, A
39	20.8	50.7	1665	4	US-09-614-221A-65	Sequence 65, Appl
40	20.8	50.7	2594	4	US-10-140-002-445	Sequence 245, App
41	20.8	50.7	2940	4	US-09-248-796A-5139	Sequence 5139, Ap
42	20.8	50.7	3585	4	US-09-270-767-14479	Sequence 14479, A
43	20.8	50.7	4825	6	5459251-1	Patent No. 5459251
44	20.8	50.7	5086	2	US-08-465-485A-19	Sequence 19, Appl
45	20.8	50.7	5086	2	US-08-365-486A-14	Sequence 14, Appl
46	20.8	50.7	5086	3	US-09-060-285-19	Sequence 19, Appl
47	20.8	50.7	5086	3	US-08-880-342-14	Sequence 14, Appl
48	20.8	50.7	5086	4	US-09-724-426-19	Sequence 19, Appl
49	20.8	50.7	5086	4	US-09-233-527-7	Sequence 7, Appl
50	20.8	50.7	5086	5	PCT-US93-05651-4	Sequence 4, Appl
51	20.8	50.7	5086	5	PCT-US93-06251-2	Sequence 2, Appl
52	20.8	50.7	5094	3	US-09-224-186-7	Sequence 7, Appl
53	20.8	50.7	5104	6	5506344-1	Patent No. 5506344
54	20.8	50.7	16656	4	US-09-433-579-3	Sequence 3, Appl
55	20.8	50.7	38844	3	US-09-734-675-3	Sequence 3, Appl
56	20.8	50.7	148567	4	US-09-801-876B-3	Sequence 3, Appl
57	20.8	50.7	148567	4	US-10-254-869-3	Sequence 3, Appl
58	20.8	50.7	580073	4	US-08-545-528D-1	Sequence 1, Appl
59	20.8	50.7	1664976	4	US-08-916-421B-1	Sequence 1, Appl
60	20.6	50.2	237	4	US-09-682-570-1	Sequence 1, Appl
61	20.6	50.2	242	4	US-09-248-796A-7725	Sequence 7725, Ap
62	20.6	50.2	414	4	US-09-513-999C-9073	Sequence 9073, Ap
63	20.6	50.2	414	4	US-09-248-796A-5571	Sequence 5571, Ap
64	20.6	50.2	1569	2	US-08-743-637B-176	Sequence 176, App
65	20.6	50.2	1569	3	US-08-526-840B-176	Sequence 176, App
66	20.6	50.2	4612	4	US-09-023-655-956	Sequence 956, App
67	20.6	50.2	1230025	4	US-09-198-452A-1	Sequence 1, Appl
68	20.6	50.2	1664976	4	US-08-916-421B-1	Sequence 1, Appl
69	20.4	49.8	201	4	US-09-248-796A-13699	Sequence 13699, A
70	20.4	49.8	665	3	US-09-030-607-196	Sequence 196, App
71	20.4	49.8	665	3	US-09-439-313-196	Sequence 196, App
72	20.4	49.8	665	3	US-09-352-816A-196	Sequence 196, App
73	20.4	49.8	665	4	US-09-232-149A-196	Sequence 196, App
74	20.4	49.8	665	4	US-09-159-812-196	Sequence 196, App
75	20.4	49.8	665	4	US-09-636-215-196	Sequence 196, App
76	20.4	49.8	665	4	US-09-685-166A-196	Sequence 196, App
77	20.4	49.8	665	4	US-09-115-453-196	Sequence 196, App
78	20.4	49.8	665	4	US-09-688-489-196	Sequence 196, App
79	20.4	49.8	665	4	US-09-679-426-196	Sequence 196, App
80	20.4	49.8	665	4	US-09-786-480B-6	Sequence 6, Appl
81	20.4	49.8	979	4	US-09-546-986A-7	Sequence 7, Appl
82	20.4	49.8	1065	4	US-09-524-730-7	Sequence 7, Appl
83	20.4	49.8	1065	3	US-08-936-165A-135	Sequence 135, App
84	20.4	49.8	2517	4	US-09-857-556A-11	Sequence 11, Appl
85	20.4	49.8	4406	1	US-08-369-043-1	Sequence 1, Appl
86	20.4	49.8	5152	4	US-10-204-708-48	Sequence 48, Appl
87	20.4	49.8	64467	4	US-09-801-671B-3	Sequence 3, Appl
88	20.4	49.8	118959	4	US-09-791-105B-32	Sequence 32, Appl
89	20.4	49.8	186399	4	US-09-734-674-3	Sequence 3, Appl
90	20.4	49.8	202001	4	US-09-557-884-1	Sequence 1, Appl
91	20.4	49.8	1830121	4	US-09-643-990A-1	Sequence 1, Appl
92	20.4	49.8	1830121	4	US-10-339-960-1	Sequence 1, Appl
93	20.4	49.8	1830121	4	US-09-270-767-30830	Sequence 30830, A
94	20.2	49.3	207	4	US-09-270-767-2044	Sequence 204, App
95	20.2	49.3	973	4	US-09-270-767-15486	Sequence 15486, A
96	20.2	49.3	973	4	US-09-270-767-14621	Sequence 14621, A
97	20.2	49.3	991	4	US-09-248-796A-1305	Sequence 1305, App
98	20.2	49.3	1059	4	US-09-134-078-3	Sequence 3, Appl
99	20.2	49.3	1266	3	US-09-134-078-3	Sequence 666, App
100	20.2	49.3	1662	4	US-09-134-000C-666	

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OW nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:35:05 ; Search time 177.265 Seconds  
(without alignments)  
1214.152 Million cell updates/sec

Title: US-10-035-833A-7074

Perfect score: 1 tctccatagtgtaaaaaaa.....gtccaccaatagtggaat 41

Sequence: IDENTITY\_NUC  
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Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	41	100.0	3785	3	AAFI8025	Lung	Canc
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4	41	100.0	5102	6	ABK54488	Human	end
5	41	100.0	5102	6	ABL62883	Breast	ca
6	41	100.0	5102	6	ABK64720	Human	ben
7	41	100.0	5102	6	AAI39861	Human	all
8	41	100.0	5102	10	ADP14611	Human	src
9	41	100.0	5102	10	ACG46768	Human	CDP
10	41	100.0	5102	11	AD132100	Human	CDN
11	41	100.0	5128	6	ABV78036	Human	CDN
12	41	100.0	5128	6	ABV77942	Hypoxia-r	
13	41	100.0	5128	6	ACF34492	Gene	enco
14	41	100.0	5128	8	ACC50124	Breast	ca
15	41	100.0	5128	12	ADN03862	Antipsoi	
16	41	100.0	5134	6	ABK88882	Human	CYP
17	41	100.0	5329	6	AA594902	Human	DNA
18	41	100.0	10254	6	ABN81206	Human	CYP
19	29.8	72.7	297	4	AAI25712	Human	brc
20	29.8	72.7	307	4	AAI26762	Human	brc
21	29.8	72.7	311	4	AAI18107	Human	brc

22	29.6	72.7	365	4	AAI07966	Human	brc
23	26.6	64.9	5371	4	AA546799	Tumour	su
24	58.5	3355	10	ADDE4106	Human	gen	
25	58.5	3355	10	ADDE4110	Human	gen	
26	58.5	335913	5	AAI61371	Soybean	2	
27	58.5	335913	5	AAI61372	Soybean	2	
28	58.0	2050	2	AAK97997	Human	sec	
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:40:10 : Search time 720.113 Seconds  
(without alignments)  
2692.464 Million cell updates/sec

Title: US-10-035-833a-7074  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues  
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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3: gb\_in:\*  
4: gb\_cm:\*  
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9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vt:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	41	100.0	5102	6	AR380881 Sequence
6	41	100.0	5102	6	AX330711 Sequence
7	41	100.0	5102	6	AX663644 Sequence
8	41	100.0	5102	6	BD169898 Method to
9	41	100.0	5102	6	HSU03688
10	41	100.0	5104	6	CO714214 Sequence
11	41	100.0	5134	6	AX666071 Sequence
12	41	100.0	5234	11	BY177879
13	41	100.0	5329	6	AX281748 Sequence
14	41	100.0	12124	9	AY393998 Homo sapi
15	41	100.0	12177	9	HSU56438
16	41	100.0	79303	2	AC011074 Homo sapi
17	41	100.0	209156	9	AC009229 Homo sapi
18	41	100.0	211222	2	AC022097 Homo sapi
19	40	97.6	41	6	AX520876 Sequence

20	31	75.6	3124	11	G06772
21	29.8	72.7	297	6	CO433148
22	29.8	72.7	307	6	CO434199
23	29.8	72.7	311	6	CO425540
24	29.8	72.7	365	6	CO415389
25	27.8	67.8	65118	2	AC084187
26	27.8	67.8	131682	9	AL672277
27	26.8	65.4	173525	2	AC067893
28	26.8	65.4	184585	2	AC079465
29	26.8	65.4	184649	2	AC025185
30	26.6	64.9	5371	6	AX251557
31	26.6	64.9	149442	10	AC116180
32	26.6	64.9	169766	10	AC147631
33	26.6	64.9	173198	9	AC108132
34	26.2	63.9	157775	2	AC102331
35	26.2	63.9	161741	8	AC120535
36	26.2	63.9	170020	8	AC138001
37	25.8	62.9	5830	8	AY158836
38	25.8	62.9	139280	9	AC099052
39	25.8	62.9	171461	9	AC097041
40	25.8	62.9	185161	9	AC006059
41	25.8	62.9	194742	9	AC092047
42	25.6	62.4	128074	8	AC145165
43	25.6	62.4	143254	5	BX649263
44	25.6	62.4	145342	2	AC023220
45	25.6	62.4	145342	2	AC023220
46	25.6	62.4	145342	2	AC023220
47	25.6	62.4	161790	2	AC023271
48	25.6	62.4	169327	5	BX957258
49	25.6	62.4	201088	9	ALU859733
50	25.6	62.4	228377	2	EX897723
51	25.6	62.4	230856	2	AC133817
52	25.6	62.4	234077	2	AC130857
53	25.6	62.4	259063	2	AC113390
54	25.4	62.0	197911	10	ALU805957
55	25.4	62.0	223873	2	AC107198
56	25.4	62.0	224436	2	AC107405
57	25.4	62.0	231404	2	AC127772
58	25.4	62.0	233342	2	AC096410
59	25.4	62.0	238565	2	AC096802
60	25.2	61.5	337	11	G12267
61	25.2	61.5	114707	2	AC146332
62	25.2	61.5	132745	2	AC068647
63	25.2	61.5	139435	2	AC068635
64	25.2	61.5	140556	2	AC078807
65	25	61.0	97734	9	AC095066
66	25	61.0	127148	2	AP002081
67	25	61.0	145246	10	AC115906
68	25	61.0	147519	2	AC079099
69	25	61.0	155584	5	EX294385
70	25	61.0	164271	2	AC009571
71	25	61.0	169604	2	BX640595
72	25	61.0	175131	10	AC127681
73	25	61.0	181230	5	EX296556
74	25	61.0	191261	2	AC111828
75	25	61.0	217266	10	AC124177
76	25	61.0	222162	10	AC109281
77	25	61.0	225655	10	AC099690
78	25	61.0	245784	10	AC099863
79	25	61.0	279425	2	AC128006
80	24.8	60.5	52000	2	AC101348
81	24.8	60.5	165098	2	AC146829
82	24.8	60.5	183543	10	AL670360
83	24.8	60.5	187604	2	AC136384
84	24.8	60.5	201262	2	AC118512
85	24.8	60.5	203300	9	AC008744
86	24.8	60.5	218882	2	AC148459
87	24.6	60.0	339503	2	AC101063
88	24.6	60.0	134608	2	AC146839
89	24.6	60.0	137475	5	BX005277
90	24.6	60.0	174866	2	BX510916
91	24.6	60.0	182715	2	AC130031
92	24.6	60.0	183068	2	CR354422

G06772	human	STS	W
CO433148	Sequence		
CO434199	Sequence		
CO425540	Sequence		
CO415389	Sequence		
AC084187	Homo sapi		
AL672277	Human DNA		
AC067893	Homo sapi		
AC079465	Homo sapi		
AC025185	Homo sapi		
AX251557	Sequence		
AC116180	Mus muscu		
AC147631	Mus muscu		
AC108132	Mus muscu		
AC102331	Mus muscu		
AC120535	Oryza sat		
AC138001	Oryza sat		
AY158836	Fraxaria		
AC099052	Homo sapi		
AC097041	Homo sapi		
AC006059	Homo sapi		
AC092047	Homo sapi		
AC145165	Medicago		
BX649263	Zebrafish		
AC023220	Homo sapi		
AC023220	Homo sapi		
AC023271	Homo sapi		
BX957258	Zebrafish		
ALU859733	Human DNA		
AC128805	Rattus no		
EX897723	Danio rer		
AC133817	Rattus no		
AC130857	Rattus no		
AC113390	Rattus no		
ALU805957	Mouse DNA		
AC107198	Rattus no		
AC107405	Rattus no		
AC127772	Rattus no		
AC096410	Rattus no		
AC096802	Rattus no		
G12267	UNH114 Tila		
AC146332	Medicago		
AC068647	Homo sapi		
AC068635	Homo sapi		
AC078807	Homo sapi		
AC095066	Homo sapi		
AP002081	Homo sapi		
AC115906	Mus muscu		
AC079099	Homo sapi		
BX294385	Zebrafish		
AC009571	Homo sapi		
BX640595	Danio rer		
AC127681	Mus muscu		
EX296556	Zebrafish		
AC111828	Rattus no		
AC124177	Mus muscu		
AC109281	Mus muscu		
AC099690	Mus muscu		
AC099863	Mus muscu		
AC128006	Rattus no		
AC101348	Mus muscu		
AC146829	Papio anu		
AL670360	Mouse DNA		
AC136384	Rattus no		
AC008744	Homo sapi		
AC148459	Xenopus t		
AC101063	Mus muscu		
AC146839	Dasytus n		
BX005277	Zebrafish		
BX510916	Zebrafish		
AC130031	Rattus no		
CR354422	Danio rer		

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:11:10 : Search time 1452.89 Seconds  
(without alignments)  
1028.317 Million cell updates/sec

Title: US-10-035-833a-7073

Perfect score: 41  
Sequence: 1 tcagcaagaagaaaaa.....gccagccaagcttaacta 41

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	580	7	W02900 zac0407.r1
2	41	100.0	585	1	AI536104 x06.p9.f9
3	36	87.8	201	7	W03094 za0307.r1
4	32.8	80.0	663	5	BU686928 UI-CF-D01
5	31.8	77.6	339	2	BE925815 QV0-BN004
6	30.2	73.7	225	2	AW999474 MRO-BN007
7	29.4	71.7	409	6	CD698653 EST15176
8	28	68.3	1004	4	BI522407 603081321
9	27.4	66.8	374	7	CP431938 NIT1_16.H
10	27.4	66.8	365	7	CN682584 E0166G06-
11	27.4	66.8	815	5	BX689954 BX689954
12	27.2	66.3	621	8	AQ373554 RPCI1.1-15
13	27.2	66.3	745	4	BG531495 602561679
14	27.2	66.3	881	8	AZ753829 RPCI-24-1
15	27.2	66.3	1131	8	CC208497 CC208497
16	27	65.9	350	9	CE177608 t1gr-g8b-
17	27	65.9	823	5	BU218198 603105762
18	27	65.9	845	8	CC389109 PTHB86TD
19	27	65.9	906	9	CL117859 t8B1-69F2
20	26.8	65.4	286	1	AA185458 tm47a08.r
21	26.8	65.4	447	5	BY541727 BY541727
22	26.8	65.4	447	1	AA597168 v024a09.r
23	26.8	65.4	635	5	BQ206621 UI-R-D21-
24	26.8	65.4	687	9	CC957683 BO1B0677R

C	25	26.8	65.4	690	7	CN438494
C	26	26.8	65.4	782	9	AG439136 Mus_muscu
C	27	26.6	64.9	610	5	BX694247 BX694247
C	28	26.6	64.9	729	9	CR077759 Reverse.s
C	29	26.6	64.9	774	7	CR427047 CR427047
C	30	26.6	64.9	807	5	BX687032 BX687032
C	31	26.6	64.9	808	5	BX701131 BX701131
C	32	26.6	64.9	809	5	BX686008 BX686008
C	33	26.6	64.9	811	5	CC522028 CC522028
C	34	26.6	64.9	814	5	BX693986 BX693986
C	35	26.4	64.4	388	8	AZ966084 AZ966084
C	36	26.4	64.4	763	9	CC560820 CC560820
C	37	26.4	64.4	958	5	BQ723128 BQ723128
C	38	26.4	64.4	1200	3	CR698500 CR698500
C	39	26.2	63.9	137	6	CB913091 CB913091
C	40	26.2	63.9	182	9	CG790081 CG790081
C	41	26.2	63.9	466	8	AZ345022 AZ345022
C	42	26.2	63.9	506	9	CG977564 CG977564
C	43	26.2	63.9	648	6	CD714444 CD714444
C	44	26.2	63.9	733	9	CL795859 CL795859
C	45	26.2	63.9	929	9	CNS051KY CNS051KY
C	46	26.2	63.9	180	1	AV065791 AV065791
C	47	26	63.4	437	7	CF897830 CF897830
C	48	26	63.4	182	1	AU038880 AU038880
C	49	26	63.4	225	2	BB211238 BB211238
C	50	26	63.4	281	1	AV070719 AV070719
C	51	26	63.4	295	5	AV068825 AV068825
C	52	26	63.4	382	5	BY540891 BY540891
C	53	26	63.4	386	1	AV066924 AV066924
C	54	26	63.4	430	1	AA915406 AA915406
C	55	26	63.4	437	7	CF897830 CF897830
C	56	26	63.4	443	2	AW763630 AW763630
C	57	26	63.4	493	1	AI020196 AI020196
C	58	26	63.4	548	8	BH859469 BH859469
C	59	26	63.4	548	4	BG144175 BG144175
C	60	26	63.4	605	8	AZ842743 AZ842743
C	61	26	63.4	642	2	BE336468 BE336468
C	62	26	63.4	694	5	BP149851 BP149851
C	63	26	63.4	785	7	CK031740 CK031740
C	64	26	63.4	833	5	BU362978 BU362978
C	65	26	63.4	882	6	CA470932 CA470932
C	66	26	63.4	1027	4	BG519054 BGS19054
C	67	26	63.4	1143	5	AX463464 AX463464
C	68	25.8	62.9	288	5	BY545680 BY545680
C	69	25.8	62.9	390	5	EX615697 EX615697
C	70	25.8	62.9	443	2	AW532503 AW532503
C	71	25.8	62.9	551	6	CA917438 CA917438
C	72	25.8	62.9	560	4	BG451579 BG451579
C	73	25.8	62.9	582	8	AZ214547 AZ214547
C	74	25.8	62.9	594	4	AZ361610 AZ361610
C	75	25.8	62.9	605	9	CE628694 CE628694
C	76	25.8	62.9	654	4	E1267962 E1267962
C	77	25.8	62.9	699	9	AG168824 AG168824
C	78	25.8	62.9	769	9	AG460018 AG460018
C	79	25.8	62.9	863	8	AZ683057 A2683057
C	80	25.8	62.9	863	8	BZ848780 BZ848780
C	81	25.8	62.9	892	6	BZ848742 BZ848742
C	82	25.8	62.9	941	6	CD795914 CD795914
C	83	25.8	62.9	1037	9	CNS01780 CNS01780
C	84	25.6	62.4	349	7	CK727545 CK727545
C	85	25.6	62.4	364	1	AA233852 z641C09.s
C	86	25.6	62.4	410	4	BM032337 BM032337
C	87	25.6	62.4	417	1	AJ688430 AJ688430
C	88	25.6	62.4	424	1	CB796172 CB796172
C	89	25.6	62.4	466	1	AI694480 AI694480
C	90	25.6	62.4	498	4	BM254648 BM254648
C	91	25.6	62.4	498	7	CK291515 CK291515
C	92	25.6	62.4	515	9	CE727174 C1gr-g8s-
C	93	25.6	62.4	525	5	BY365254 BY365254
C	94	25.6	62.4	534	8	BH457700 BQGD05TF
C	95	25.6	62.4	554	2	BF224042 BF224042
C	96	25.6	62.4	555	8	AQ414660 AQ414660
C	97	25.6	62.4	599	5	BX470609 BX470609

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 09:56:20 : Search time 158.775 Seconds  
(without alignments)  
1324.090 Million cell updates/sec

Title: US-10-035-833a-7073

Perfect score: 41  
Sequence: 1 tcagcaagaagaaaaaa.....gccagccaagcttaatra 41

Scoring table:  
Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications: NA.\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
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6: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
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15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
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20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	41	16 US-10-035-833a-7073	Sequence 7077, Ap
2	41	100.0	533	13 US-10-027-632-245152	Sequence 245152, Ap
3	41	100.0	533	13 US-10-027-632-245153	Sequence 245153, Ap
4	41	100.0	533	15 US-10-027-632-245152	Sequence 245152, Ap
5	41	100.0	533	15 US-10-027-632-245153	Sequence 245153, Ap
6	41	100.0	2181	10 US-09-999-686-10	Sequence 10, Appl
7	41	100.0	2721	10 US-09-999-686-12	Sequence 12, Appl
8	41	100.0	3118	10 US-09-999-686-19	Sequence 19, Appl
9	41	100.0	5102	9 US-09-919-497-8	Sequence 8, Appl
10	41	100.0	5102	9 US-09-954-531-153	Sequence 153, Appl
11	41	100.0	5102	10 US-09-960-706-938	Sequence 938, Appl
12	41	100.0	5102	10 US-09-873-519-615	Sequence 615, Appl

13	41	100.0	5102	15 US-10-204-752-36	Sequence 36, Appl
14	41	100.0	5102	16 US-10-641-643-1426	Sequence 1426, Ap
15	41	100.0	5102	17 US-10-775-169-230	Sequence 230, Appl
16	41	100.0	5128	15 US-10-177-293-95	Sequence 95, Appl
17	41	100.0	5128	15 US-10-170-385-126	Sequence 126, Appl
18	41	100.0	5128	15 US-10-170-385-326	Sequence 326, Appl
19	41	100.0	5128	15 US-10-172-118-433	Sequence 433, Appl
20	41	100.0	5128	16 US-10-342-887-433	Sequence 433, Appl
21	41	100.0	5134	10 US-09-999-686-1	Sequence 1, Appl
22	41	100.0	5329	15 US-10-240-965-157	Sequence 157, Appl
23	40.6	99.0	3785	9 US-09-925-302-44	Sequence 44, Appl
24	40.6	99.0	3785	10 US-09-925-302-44	Sequence 44, Appl
25	36.2	88.3	23415	16 US-10-052-482-49	Sequence 18261, A
26	27.6	67.3	83450	10 US-09-811-469-3	Sequence 49, Appl
27	27	65.9	83450	10 US-09-811-469-3	Sequence 3, Appl
28	26.5	64.9	15832	15 US-10-239-676-105	Sequence 105, Appl
29	26.5	64.9	15832	15 US-10-240-453-117	Sequence 117, Appl
30	26.5	64.9	15832	15 US-10-027-632-288971	Sequence 288971, Appl
31	26.6	63.4	554	13 US-10-027-632-288971	Sequence 288971, Appl
32	26	63.4	554	15 US-10-052-482-50	Sequence 50, Appl
33	26	63.4	9261	16 US-10-424-599-74567	Sequence 11631, A
34	26	63.4	9261	16 US-10-425-114-10598	Sequence 10598, A
35	25.6	62.4	183999	17 US-10-322-696-34	Sequence 12563, A
36	25.6	62.4	357652	10 US-09-918-995-12563	Sequence 23631, A
37	25.4	62.0	413	16 US-10-424-599-74567	Sequence 5668, Ap
38	25.4	62.0	2176	17 US-10-741-601-5668	Sequence 11631, A
39	25.4	62.0	165156	16 US-10-424-599-74570	Sequence 74570, A
40	25.2	61.5	178	16 US-10-424-599-74570	Sequence 12846, A
41	25	61.0	683	16 US-10-425-114-10598	Sequence 10598, A
42	25	61.0	825	16 US-10-424-599-74567	Sequence 74567, A
43	25	61.0	1101	16 US-10-437-863-63121	Sequence 63121, A
44	25	61.0	3759	17 US-09-997-722-136	Sequence 136, Appl
45	25	61.0	40955	11 US-10-189-267-20	Sequence 20, Appl
46	25	61.0	98686	13 US-10-087-192-1834	Sequence 1834, Appl
47	25	61.0	152330	16 US-09-918-995-15859	Sequence 15859, A
48	24.8	60.5	497	16 US-10-242-5358-43684	Sequence 43684, A
49	24.8	60.5	497	16 US-10-085-7834-43684	Sequence 43684, A
50	24.8	60.5	497	16 US-10-027-632-269156	Sequence 269156, A
51	24.8	60.5	497	16 US-10-027-632-269157	Sequence 269157, A
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55	24.8	60.5	598	15 US-10-027-632-269157	Sequence 269157, A
56	24.8	60.5	598	15 US-10-027-632-114287	Sequence 114287, A
57	24.8	60.5	3030	13 US-10-027-632-114288	Sequence 114288, A
58	24.8	60.5	3030	15 US-10-027-632-114287	Sequence 114287, A
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60	24.8	60.5	3030	15 US-10-027-632-114287	Sequence 114287, A
61	24.8	60.5	69652	17 US-10-322-281-72	Sequence 72, Appl
62	24.6	60.0	392	9 US-09-983-965-4284	Sequence 4284, Appl
63	24.6	60.0	549	16 US-10-424-599-47467	Sequence 47467, A
64	24.6	60.0	559	16 US-10-424-599-47467	Sequence 47467, A
65	24.6	60.0	889	13 US-10-027-632-172535	Sequence 172535, A
66	24.6	60.0	889	13 US-10-027-632-172536	Sequence 172536, A
67	24.6	60.0	889	13 US-10-027-632-172535	Sequence 172535, A
68	24.6	60.0	889	15 US-10-027-632-172536	Sequence 172536, A
69	24.6	60.0	5081	15 US-10-128-714-156	Sequence 156, Appl
70	24.6	60.0	5311	15 US-10-128-714-156	Sequence 156, Appl
71	24.6	60.0	1000	15 US-10-633-843-10	Sequence 10, Appl
72	24.6	60.0	41966	16 US-10-027-632-18917	Sequence 18917, A
73	24.6	60.0	45364	17 US-10-332-811-235	Sequence 235, Appl
74	24.4	59.5	500	15 US-10-029-386-7906	Sequence 7906, Appl
75	24.4	59.5	539	13 US-10-027-632-4931	Sequence 4931, Appl
76	24.4	59.5	539	13 US-10-027-632-4931	Sequence 4931, Appl
77	24.4	59.5	540	13 US-10-027-632-18917	Sequence 18917, A
78	24.4	59.5	540	13 US-10-027-632-18917	Sequence 18917, A
79	24.4	59.5	540	13 US-10-027-632-18917	Sequence 18917, A
80	24.4	59.5	540	13 US-10-027-632-18917	Sequence 18917, A
81	24.4	59.5	540	13 US-10-027-632-18917	Sequence 18917, A
82	24.4	59.5	1119	16 US-10-282-1224-22973	Sequence 22973, A
83	24.4	59.5	97415	17 US-10-322-281-308	Sequence 308, Appl
84	24.2	59.0	180227	17 US-10-322-281-308	Sequence 308, Appl
85	24.2	59.0	457	14 US-10-060-036-1577	Sequence 1577, Appl
	24.2	59.0	481	16 US-10-424-599-114135	Sequence 114135, A



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OM nucleic - nucleic search, using SW model

Run on: October 31, 2004, 08:13:20 ; Search time 37.1834 Seconds  
(without alignments)  
783.789 Million cell updates/sec

Title: US-10-035-833a-7073

Perfect score: 41  
Sequence: 1 tcagcaagaaaaa.....gccagcagcttaatra 41

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A.COMB.seg:\*
- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seg:\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seg:\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seg:\*
- 5: /cgn2\_6/ptodata/1/ina/PCPUS.COMB.seg:\*
- 6: /cgn2\_6/ptodata/1/ina/backfile1.seg:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	41	100.0	5102	4	US-09-023-655-1426
2	41	100.0	5102	4	US-09-919-497-8
3	27	65.9	83450	4	US-09-811-469-3
4	27	65.9	83450	4	US-10-370-659-3
5	24	58.5	1426	4	US-09-023-655-375
6	23.8	58.0	894	4	US-09-134-000C-211
7	23.4	57.1	195	4	US-09-621-976-14748
8	23.4	57.1	567	4	US-09-543-681A-622
9	23.4	57.1	645	4	US-09-385-982-40
10	23.2	56.6	445	4	US-09-270-767-4909
11	23.2	56.6	445	4	US-09-270-767-20191
12	23.2	56.6	2182	3	US-09-039-046-3
13	23.2	56.6	5666	4	US-10-204-708-30
14	23	56.1	328	4	US-09-621-976-13643
15	23	56.1	396	4	US-09-513-999C-12076
16	23	56.1	1089	4	US-09-248-796A-461
17	23	56.1	8705	4	US-09-544-398B-10
18	23	56.1	8705	4	US-09-544-771-10
19	23	56.1	9347	4	US-10-204-708-36
20	23	56.1	786431	4	US-09-751-389-3
21	22.8	55.6	469	4	US-09-134-000C-3073
22	22.8	55.6	469	4	US-09-270-767-14304
23	22.8	55.6	601	3	US-09-814-951A-14
24	22.8	55.6	1187	4	US-09-963-665-7
25	22.8	55.6	1187	4	US-09-963-333-7
26	22.8	55.6	1187	4	US-09-963-677-7
27	22.8	55.6	9704	3	US-09-814-951A-3

28	22.8	55.6	18596	3	US-09-318-448-11	Sequence 11, Appl
29	22.8	55.6	18597	4	US-09-962-665-8	Sequence 8, Appl
30	22.8	55.6	18597	4	US-09-963-333-8	Sequence 8, Appl
31	22.8	55.6	18597	4	US-09-962-677-8	Sequence 4, Appl
32	22.6	55.1	547	2	US-08-111-365B-41	Sequence 41, Appl
33	22.6	55.1	1801	1	US-08-668-123-41	Sequence 1, Appl
34	22.6	55.1	1801	1	US-08-557-917A-1	Sequence 1, Appl
35	22.6	55.1	1801	3	US-09-084-153-1	Sequence 1, Appl
36	22.6	55.1	1801	3	US-09-084-079-1	Sequence 1, Appl
37	22.6	55.1	4698	1	US-07-807-043B-5	Sequence 5, Appl
38	22.6	55.1	4698	1	US-08-299-849B-5	Sequence 5, Appl
39	22.6	55.1	4698	2	US-08-142-368A-5	Sequence 5, Appl
40	22.6	55.1	4698	3	US-08-967-727-5	Sequence 5, Appl
41	22.6	55.1	4698	3	US-08-037-310D-5	Sequence 5, Appl
42	22.6	55.1	4698	4	US-09-593-850-5	Sequence 5, Appl
43	22.6	55.1	4698	4	US-09-579-197-5	Sequence 5, Appl
44	22.6	55.1	4698	4	US-09-404-026-5	Sequence 5, Appl
45	22.6	55.1	4698	4	US-09-312-464-5	Sequence 5, Appl
46	22.6	55.1	54945	4	US-09-620-312D-255	Sequence 255, Appl
47	22.6	55.1	54945	4	US-09-967-669-10	Sequence 10, Appl
48	22.4	54.6	214	4	US-09-513-999C-34142	Sequence 688, Ap
49	22.4	54.6	486	4	US-09-270-767-938	Sequence 22270, A
50	22.4	54.6	486	4	US-09-270-767-92270	Sequence 2760, Ap
51	22.4	54.6	648	4	US-09-134-000C-2760	Sequence 16, Appl
52	22.4	54.6	775	4	US-09-780-717-16	Sequence 10658, A
53	22.4	54.6	942	4	US-09-270-767-10658	Sequence 19, Appl
54	22.4	54.6	959	4	US-09-205-258-19	Sequence 7, Appl
55	22.4	54.6	1674	1	US-07-778-880-7	Sequence 7, Appl
56	22.4	54.6	1674	5	PCT-US93-05640-7	Sequence 7, Appl
57	22.4	54.6	1674	5	US-09-801-876B-3	Sequence 3, Appl
58	22.4	54.6	148567	4	US-10-254-869-3	Sequence 3, Appl
59	22.2	54.1	55298	4	US-09-491-356C-1	Sequence 1, Appl
60	22.2	54.1	193303	4	US-09-497-855A-37	Sequence 37, Appl
61	22.2	54.1	193303	4	US-09-497-855A-44	Sequence 44, Appl
62	22.2	53.7	39	4	US-09-632-313A-6	Sequence 6, Appl
63	22.2	53.7	39	4	US-09-921-942B-5	Sequence 5, Appl
64	22.2	53.7	117	4	US-09-404-879A-359	Sequence 359, App
65	22.2	53.7	117	4	US-09-667-857-359	Sequence 359, App
66	22.2	53.7	232	4	US-09-702-705-993	Sequence 993, App
67	22.2	53.7	232	4	US-09-736-457-993	Sequence 993, App
68	22.2	53.7	232	4	US-09-614-124B-993	Sequence 993, App
69	22.2	53.7	232	4	US-09-614-124B-993	Sequence 993, App
70	22.2	53.7	232	4	US-09-658-824-993	Sequence 993, App
71	22.2	53.7	1529	3	US-09-189-760-5	Sequence 5, Appl
72	22.2	53.7	1529	3	US-09-188-811-5	Sequence 5, Appl
73	22.2	53.7	1529	3	US-09-514-422-5	Sequence 5, Appl
74	22.2	53.7	2199	4	US-09-708-725A-3	Sequence 3, Appl
75	22.2	53.7	2199	4	US-09-189-760-1	Sequence 1, Appl
76	22.2	53.7	2494	3	US-09-514-422-1	Sequence 1, Appl
77	22.2	53.7	2494	3	US-08-735-609-9	Sequence 9, Appl
78	22.2	53.7	3364	2	US-08-735-609-9	Sequence 9, Appl
79	22.2	53.7	3364	2	US-09-315-372-9	Sequence 9, Appl
80	22.2	53.7	3364	3	US-09-245-497-9	Sequence 9, Appl
81	22.2	53.7	3364	3	US-09-245-497-9	Sequence 9, Appl
82	22.2	53.7	3364	3	US-09-562-919-9	Sequence 9, Appl
83	22.2	53.7	3364	4	US-09-100-703A-5	Sequence 25, Appl
84	22.2	53.7	5230	4	US-09-833-718A-5	Sequence 26, Appl
85	22.2	53.7	5230	4	US-09-100-703A-5	Sequence 27, Appl
86	22.2	53.7	5231	4	US-09-838-718A-7	Sequence 7, Appl
87	22.2	53.7	5231	4	US-09-838-718A-7	Sequence 7, Appl
88	22.2	53.7	5270	4	US-09-838-718A-8	Sequence 8, Appl
89	22.2	53.7	5270	4	US-09-838-718A-8	Sequence 8, Appl
90	22.2	53.7	5270	4	US-09-838-718A-8	Sequence 8, Appl
91	22.2	53.7	152331	3	US-09-128-153-17	Sequence 17, Appl
92	22.2	53.7	152331	3	US-09-128-153-17	Sequence 16, Appl
93	22.2	53.7	152331	3	US-09-128-153-17	Sequence 16, Appl
94	22.2	53.7	1230025	4	US-09-751-389-3	Sequence 3, Appl
95	21.8	53.2	228	4	US-09-198-452A-1	Sequence 1, Appl
96	21.8	53.2	282	4	US-09-621-976-11262	Sequence 8312, A
97	21.8	53.2	284	4	US-09-621-976-11262	Sequence 11262, A
98	21.8	53.2	366	4	US-09-621-976-11262	Sequence 1765, A
99	21.8	53.2	1281	4	US-09-248-796A-1728	Sequence 1728, Ap
100	21.8	53.2	1281	4	US-09-134-000C-1728	Sequence 3175, Ap
					US-09-134-000C-3273	Sequence 3273, Ap

CM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:35:05 ; Search time 177.265 Seconds

(without alignments)  
1214.152 Million cell updates/sec

Title: US-10-035-833A-7073

Perfect score: 41 tcagcaagaagaaaaaa.....gccagccaagcttaatta 41

Sequence: 1

Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0

Searched: 413486 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: Genesegq\_23Sep04:\*  
2: Genesegq1980s:\*  
3: Genesegq1990s:\*  
4: Genesegq2000s:\*  
5: Genesegq2001as:\*  
6: Genesegq2001bs:\*  
7: Genesegq2002as:\*  
8: Genesegq2003as:\*  
9: Genesegq2003bs:\*  
10: Genesegq2003cs:\*  
11: Genesegq2003ds:\*  
12: Genesegq2004s:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	41	6	ABZ50291 Human cyt
2	41	100.0	5102	6	ABO79929 Human cyt
3	41	100.0	5102	6	ABK35488 Human end
4	41	100.0	5102	6	ABL62883 Breast ca
5	41	100.0	5102	6	ABK64720 Human ben
6	41	100.0	5102	6	AA139861 Human a11
7	41	100.0	5102	10	ADD14611 Human str
8	41	100.0	5102	10	ACC46768 Human COP
9	41	100.0	5102	11	AD133100 Human CDN
10	41	100.0	5128	6	ABV78036 Hypoxia-r
11	41	100.0	5128	6	ABV77942 Hypoxia-r
12	41	100.0	5128	8	ACF34492 Gene enco
13	41	100.0	5128	8	ACC50124 Breast ca
14	41	100.0	5128	12	ADN03862 Antipsori
15	41	100.0	5134	6	ABK88882 Human CYP
16	41	100.0	5329	6	ABK94902 Human DNA
17	41	100.0	10254	6	ABN81206 Human CYP
18	40.6	99.0	3785	3	AA118025 Lung can
19	36.2	88.3	362	9	ACH31049 Human bon
20	27.8	67.8	11130	5	ABA16386 Human ner
21	27.6	67.3	23415	9	ADA02543 Mouse Pim

22	27.6	67.3	23415	10	ADB72281	ADB72281 Mouse Pim
23	27.6	67.3	23415	10	ADB95791	ADB95791 Mouse Pim
24	27	65.9	83450	10	AAD58977	AAD58977 Human pho
25	27	65.9	83450	10	ADG88582	ADG88582 Human pho
26	26.8	65.4	378	5	AA166163	AA166163 Novel hum
27	26.6	64.9	15832	6	AA545396	AA545396 Chemically
28	26.6	64.9	15832	6	ABL33342	ABL33342 Human imm
29	26.6	64.9	15832	6	ABK28243	ABK28243 DNA trans
30	26.4	64.4	765	4	AA119958	AA119958 Human bre
31	26	63.4	9261	9	ADA02544	ADA02544 Mouse Pim
32	26	63.4	9261	10	ADB72282	ADB72282 Mouse Pim
33	26	63.4	9261	10	ADB95792	ADB95792 Mouse DNA
34	25.6	62.4	110000	6	AB553202	Continuation (3 of
35	25.6	62.4	183999	4	AA192831	AA192831 Human ABC
36	25.6	62.4	183999	4	AB555200	AB555200 Genomic D
37	25.4	62.0	413	9	ACH25351	ACH25351 Human adu
38	25.4	62.0	670	3	AAC35461	AAC35461 Arabidops
39	25.4	62.0	177851	8	AA157272	AA157272 bA438B23-
40	25.2	61.5	457	4	AA171707	AA171707 Human imm
41	25.2	61.5	633	10	AB237826	AB237826 N. gonorr
42	25.2	61.5	633	12	ADP83382	ADP83382 Breast sp
43	25.2	61.5	5263	12	ADP83382	ADP83382 Breast sp
44	25.2	61.5	42488	4	AA166772	AA166772 Human imm
45	25	61.0	2518	10	ADD48365	ADD48365 Human gen
46	25	61.0	27780	6	ABX12674	ABX12674 Selectin
47	25	61.0	40954	10	ADP85349	ADP85349 Mouse Sel
48	25	61.0	40955	9	ADA02870	ADA02870 Human SEL
49	25	61.0	40955	10	ADP72608	ADP72608 Human car
50	25	61.0	40955	12	ADM74465	ADM74465 Human car
51	25	61.0	98686	12	AD180019	AD180019 Human cta
52	25	61.0	138169	3	AAA34791	AAA34791 Human ade
53	25	61.0	141586	11	ABD20695	ABD20695 Human pul
54	25	61.0	141586	11	AAA35005	AAA35005 Human ade
55	25	61.0	141589	3	AA135030	AA135030 Human ade
56	25	61.0	141589	3	AA121152	AA121152 Human low
57	25	61.0	141589	3	AA120913	AA120913 Human ELA
58	25	61.0	141589	3	AA121127	AA121127 Human low
59	25	61.0	141589	10	AB296821	AB296821 Human nuc
60	25	61.0	141589	10	AB296607	AB296607 Human ELA
61	25	61.0	141589	10	AB296846	AB296846 Human nuc
62	25	61.0	141589	11	ABD20670	ABD20670 Human pul
63	25	61.0	141501	11	ABD19162	ABD19162 Human ELA
64	25	61.0	146981	3	AA121442	AA121442 Human ELA
65	25	61.0	146982	10	ABD297136	ABD297136 Human ELA
66	25	61.0	146984	11	ABD19160	ABD19160 Human ELA
67	25	61.0	209273	3	AA121437	AA121437 Human fac
68	25	61.0	209274	10	AB297131	AB297131 Human enz
69	25	61.0	209284	11	ABD19790	ABD19790 Human fac
70	24.8	60.5	427	6	ABN78177	ABN78177 Human ORF
71	24.8	60.5	497	9	ACH28647	ACH28647 Human adu
72	24.8	60.5	11209	6	ABN80137	ABN80137 Human che
73	24.6	60.0	392	8	ABX54355	ABX54355 Bovine ES
74	24.6	60.0	2869	4	AB118644	AB118644 Drosophi1
75	24.6	60.0	3254	4	AB118628	AB118628 Drosophi1
76	24.6	60.0	4592	10	ADP62122	ADP62122 Human gen
77	24.6	60.0	4592	10	ADP64186	ADP64186 Human gen
78	24.6	60.0	4592	10	ADP62114	ADP62114 Human gen
79	24.6	60.0	4592	10	ADP62118	ADP62118 Human gen
80	24.6	60.0	4592	10	ADP64143	ADP64143 Human gen
81	24.6	60.0	4592	10	ADP62126	ADP62126 Human gen
82	24.6	60.0	4592	10	ADP64130	ADP64130 Human gen
83	24.6	60.0	5081	8	AB117798	AB117798 Aspergill1
84	24.6	60.0	5311	8	AB119612	AB119612 Aspergill1
85	24.6	60.0	14487	4	AB120344	AB120344 Drosophi1
86	24.6	60.0	14768	4	AB110258	AB110258 Drosophi1
87	24.6	60.0	16838	6	AA116687	AA116687 DNA encod
88	24.4	59.5	500	12	ACH74711	ACH74711 Human gen
89	24.4	59.5	829	8	AA194030	AA194030 Human neu
90	24.4	59.5	1119	8	ACA35103	ACA35103 Prokaryot
91	24.4	59.5	3587	4	AA194800	AA194800 Human ful
92	24.4	59.5	3587	12	ADL31889	ADL31889 Full leng
93	24.4	59.5	4207	8	ACC46611	ACC46611 Human dit
94	24.4	59.5	6849	4	AA172645	AA172645 Human imm

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:40:10 : Search time 720.113 Seconds  
(without alignments)  
2692.464 Million cell updates/sec

Title: US-10-035-833A-7073

Perfect score: 41  
Sequence: 1 tcagcaagaagaaaaaa.....gccagccaagccttaatta 41

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

GenBdb1:\*  
1: gb\_da:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_om:\*  
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6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	41	100.0	2181	6 AX666080 Sequence
2	41	100.0	2721	6 AX666082 Sequence
3	41	100.0	3118	6 AX666089 Sequence
4	41	100.0	5102	6 BD176699 Method of
5	41	100.0	5102	6 AR380881 Sequence
6	41	100.0	5102	6 AX330711 Sequence
7	41	100.0	5102	6 AX663644 Sequence
8	41	100.0	5102	6 BD168988 Method fo
9	41	100.0	5102	6 HSU03688 Human dioxl
10	41	100.0	5104	6 CO714214 Sequence
11	41	100.0	5134	6 AX666071 Sequence
12	41	100.0	5329	6 AX281748 Sequence
13	41	100.0	12124	9 AY393998 Homo sapi
14	41	100.0	12177	9 HSUS6438 Human dioxl
15	41	100.0	79303	2 AC011074 Homo sapi
16	41	100.0	209156	9 AC009229 Homo sapi
17	41	100.0	211222	2 AC020897 Homo sapi
18	40	97.6	41	6 AX520875 Sequence
19	30.4	74.1	139130	9 AC091504 Pan trogl

20	29.6	72.2	245182	2 AC145940	AC145940 Pan trogl
21	29.2	71.2	135119	2 AC011578	AC011578 Homo sapi
22	29.2	71.2	158817	2 AC015398	AC015398 Homo sapi
23	29	70.7	3124	11 G06772	G06772 Human SIS W
24	29	70.7	5234	11 BV177879	BV177879 sqm97309
25	28.6	69.8	219335	9 AC005015	AC005015 Mus muscu
26	28.6	69.8	219335	9 AC005015	AC005015 Homo sapi
27	28.4	69.3	174480	9 AC083903	AC083903 Homo sapi
28	28.2	68.8	139267	8 AC144592	AC144592 Medicago
29	28.2	68.8	183104	9 AL355601	AL355601 Human DNA
30	28.2	68.8	208026	9 AP006292	AP006292 Homo sapi
31	28.2	68.8	215555	2 AC133729	AC133729 Rattus no
32	28.2	68.8	225612	2 AC117641	AC117641 Mus muscu
33	28.2	68.8	310091	2 AC116258	AC116258 Rattus no
34	27.8	67.8	133336	2 AF215842	AF215842 Homo sapi
35	27.8	67.8	135572	9 AL133384	AL133384 Human DNA
36	27.8	67.8	170241	9 AC083967	AC083967 Homo sapi
37	27.6	67.3	23415	6 AX695434	AX695434 Sequence
38	27.4	66.8	87943	9 AC095064	AC095064 Homo sapi
39	27.4	66.8	154002	10 AL662902	AL662902 Mouse DNA
40	27.4	66.8	178495	2 BX510329	BX510329 Dario rer
41	27.2	66.3	116911	9 AC093019	AC093019 Homo sapi
42	27.2	66.3	120477	2 AL355995	AL355995 Homo sapi
43	27.2	66.3	134764	2 AF003305	AF003305 Homo sapi
44	27.2	66.3	155752	2 AC027557	AC027557 Homo sapi
45	27.2	66.3	162731	2 BX323452	BX323452 Dario rer
46	27.2	66.3	187728	2 AC062011	AC062011 Homo sapi
47	27.2	66.3	190441	2 AC129960	AC129960 Bos tauru
48	27.2	66.3	192001	2 AC019139	AC019139 Homo sapi
49	27	65.9	41617	9 AL603841	AL603841 Human DNA
50	27	65.9	66928	2 AC125473	AC125473 Homo sapi
51	27	65.9	83450	6 AR307588	AR307588 Sequence
52	27	65.9	83450	6 AR475456	AR475456 Sequence
53	27	65.9	102926	9 AC090829	AC090829 Homo sapi
54	27	65.9	110000	2 BX324168	BX324168 Continuation (2 of
55	27	65.9	123029	2 AF212832	AF212832 Homo sapi
56	27	65.9	178400	9 AC087481	AC087481 Homo sapi
57	27	65.9	181558	2 AC068301	AC068301 Homo sapi
58	27	65.9	187647	2 AC073220	AC073220 Homo sapi
59	27	65.9	189207	9 AC103706	AC103706 Homo sapi
60	27	65.9	196179	2 AC150717	AC150717 CalliChri
61	27	65.9	250519	2 AC094894	AC094894 Rattus no
62	27	65.9	257860	2 AC127719	AC127719 Rattus no
63	27	65.9	328117	2 AC017097	AC017097 Homo sapi
64	26.8	65.4	378	6 AX071447	AX071447 Sequence
65	26.8	65.4	60310	9 AL391647	AL391647 Human DNA
66	26.8	65.4	66224	9 AC073884	AC073884 Homo sapi
67	26.8	65.4	112602	2 AC136797	AC136797 Rattus no
68	26.8	65.4	136949	10 AL845271	AL845271 Mouse DNA
69	26.8	65.4	167974	9 AL591073	AL591073 Human DNA
70	26.8	65.4	174496	2 AC073076	AC073076 Homo sapi
71	26.8	65.4	195443	2 AC134594	AC134594 Mus muscu
72	26.8	65.4	209785	2 AC109497	AC109497 Mus muscu
73	26.8	65.4	234724	10 AL683854	AL683854 Mouse DNA
74	26.6	64.9	15832	6 AX277942	AX277942 Sequence
75	26.6	64.9	15832	6 AX323629	AX323629 Sequence
76	26.6	64.9	15832	6 AP046244	AP046244 Sequence
77	26.6	64.9	43147	9 AP002955	AP002955 Homo sapi
78	26.6	64.9	83922	8 T9A4	AT096273 Arabidops
79	26.6	64.9	99856	8 ATF24624	ATF24624 Arabidops
80	26.6	64.9	142948	9 AC147025	AC147025 Pan trogl
81	26.6	64.9	199236	2 AC109237	AC109237 Mus muscu
82	26.6	64.9	199861	8 ATCHRI29	AT161517 Arabidops
83	26.6	64.9	207890	2 AC102521	AC102521 Mus muscu
84	26.6	64.9	221879	2 AC095704	AC095704 Rattus no
85	26.6	64.9	225757	2 AC094658	AC094658 Rattus no
86	26.6	64.9	272137	2 AC095976	AC095976 Rattus no
87	26.4	64.4	765	6 CQ427391	CQ427391 Sequence
88	26.4	64.4	4081	9 HSM806464	BX538230 Homo sapi
89	26.4	64.4	14771	10 AL929432	AL929432 Mouse DNA
90	26.4	64.4	27543	10 AB126081	AB126081 Homo sapi
91	26.4	64.4	82059	9 AC130896	AC130896 Homo sapi
92	26.4	64.4	123520	9 HSU447821	AL050336 Human DNA

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:11:10 ; Search time 1417.45 Seconds  
(without alignments)  
1028.317 Million cell updates/sec

Title: US-10-035-833A-7071  
Perfect score: 40  
Sequence: 1 agctcttgagagatcttttgcagtaagactaaagggc 40

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hrc: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	* Match Length	ID	Description
1	40	100.0	717 5	EM997179 UI-H-ED0-
2	39	97.5	630 5	EM995447 UI-H-ED0-
3	35.4	88.5	627 6	CB851415 UI-CF-DU1
4	34	85.0	958 5	BO723128 AGENCOURT
5	29	72.5	403 6	CA123715 K-EST0172
6	29	72.5	579 6	CB160042 K-EST0219
7	29	72.5	592 1	AV717361 AV717361
8	29	72.5	595 4	EM713769 UI-E-ED0-
9	29	72.5	721 4	EM676467 UI-E-ED0-
10	29	72.5	934 4	BG113583 602284061
11	28	70.0	707 5	BO020105 UI-H-ED0-
12	27.8	69.5	465 5	BU689794 UI-CF-FNO
13	26.8	64.5	1270 8	BZ555833 Pacc1-60-
14	25.2	63.0	391 1	A1974443 T110391e
15	24.8	62.0	793 4	BG78374 60266527
16	24.2	60.5	953 9	CNS03X9A Tetraodon
17	23.8	59.5	458 8	CR653825 Tetraodon
18	23.8	59.5	1056 8	BZ450004 BONEV88TR
19	23.8	59.5	1056 8	CR634022 Tetraodon
20	23.8	59.5	1091 3	CR649663 Tetraodon
21	23.8	59.5	1117 3	CR634778 Tetraodon
22	23.8	59.5	1115 3	CR637710 Tetraodon
23	23.8	59.5	1167 3	CR655543 Tetraodon
24	23.8	59.5	1170 3	CR649639 Tetraodon

25	23.8	59.5	1171 3	CR635466 Tetraodon
26	23.8	59.5	1174 3	CR641445 Tetraodon
27	23.8	59.5	1200 3	CR640695 Tetraodon
28	23.8	59.5	1202 3	CR645853 Tetraodon
29	23.8	59.5	1219 3	CR644557 Tetraodon
30	23.6	59.0	464 6	CAS57970 K0235H03-
31	23.6	59.0	591 7	CN701987 E0456G01-
32	23.6	59.0	595 7	CNS30307 UI-M-H00-
33	23.6	59.0	635 7	CM698454 E0408A10-
34	23.6	59.0	635 7	CNS30701 UI-M-H00-
35	23.6	59.0	681 7	CE749554 UI-M-H00-
36	23.6	59.0	705 7	CE733941 UI-M-H00-
37	23.6	59.0	802 4	B1650633 603312046
38	23.6	59.0	813 4	B1250633 602993702
39	23.6	59.0	862 6	B2208073 CR230-330
40	23.4	58.5	485 4	BT403019 MT-P-CP1-
41	23.4	58.0	213 9	CE673711 t1gr-gss-
42	23.2	58.0	282 9	AL765931 Ardicops
43	23.2	58.0	622 8	BH732308 BOMFB0TR
44	23.2	58.0	671 9	CR206141 Reverse s
45	23.2	58.0	1436 9	CM647577 CH213-142
46	23	57.5	701 8	CC073395 CSU-K33F
47	23	57.5	782 4	B6620617 602619787
48	23	57.5	1029 2	B8885694 601508903
49	22.8	57.0	300 8	AQ261554 C1TBI-E1-
50	22.8	57.0	517 8	AQ195502 RPCI11-60
51	22.8	57.0	745 9	CU009111 ZMMBBD054
52	22.8	57.0	800 8	BZ526318 OGAKC44TC
53	22.8	57.0	852 8	BZ533595 OGAKB93TC
54	22.8	57.0	863 8	CC584681 CH240-381
55	22.8	57.0	1125 8	CC263798 CH261-211
56	22.6	56.5	431 8	B86718 CTT-HSP-201
57	22.6	56.5	443 8	B2265295 CH230-274
58	22.6	56.5	447 8	A2268949 RPCI-23-1
59	22.6	56.5	456 8	AQ228961 HS-2013 B
60	22.6	56.5	483 8	B66674 CTT-HSP-201
61	22.6	56.5	513 8	A2789872 2M0038012
62	22.6	56.5	560 1	A1897462 EST766905
63	22.6	56.5	575 1	A1486819 EST145141
64	22.6	56.5	578 9	CC956674 BO1A15TF
65	22.6	56.5	591 5	BO551403 H4009A11-
66	22.6	56.5	591 1	AL643034 AL643034
67	22.6	56.5	658 8	BH511990 BOMH52TR
68	22.6	56.5	672 7	CP742552 UI-M-HR0-
69	22.6	56.5	685 7	CN081464 EC2BBA19C
70	22.6	56.5	695 8	A2087760 RPCI-23-3
71	22.6	56.5	697 9	AG330950 Mus muscu
72	22.6	56.5	714 1	AL650479 AL650479
73	22.6	56.5	733 8	BH604717 BOHTW47TF
74	22.6	56.5	740 8	AQ307280 HS-2013 A
75	22.6	56.5	771 5	CG330635 PUTK099TD
76	22.6	56.5	832 5	BO859601 AGENCOURT
77	22.6	56.5	862 8	BZ975451 PUGJA31TB
78	22.6	56.5	865 8	BZ975457 PUGJA31TB
79	22.6	56.5	877 5	BU899871 AGENCOURT
80	22.6	56.5	893 5	CG444808 OGAEHL1TV
81	22.6	56.5	910 8	CG387817 PUBHJ13TD
82	22.6	56.5	914 9	CG230657 OGMO83TH
83	22.6	56.5	915 9	CG770721 TCBA3-2C
84	22.6	56.5	942 9	CG544472 PUK161TD
85	22.6	56.5	985 4	BG504138 602552663
86	22.6	56.5	1180 8	CC277420 CH261-67N
87	22.6	56.5	1198 8	AC441632 Mus muscu
88	22.4	56.0	315 8	AQ982177 RPCI-23-3
89	22.4	56.0	364 8	AZ051795 RPCI-23-3
90	22.4	56.0	384 8	AZ299952 RPCI-23-1
91	22.4	56.0	481 8	AZ254047 ZM0219L04
92	22.4	56.0	581 8	BZ095200 CR230-221
93	22.4	56.0	598 8	CE347992 t1gr-gss-
94	22.4	56.0	627 8	AC974445 RPCI-23-3
95	22.4	56.0	642 8	BH094655 RPCI-24-2
96	22.4	56.0	650 9	CA741597 w1a1c PKO
97	22.4	56.0	800 9	CG936647 MBEXK72TF

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 09:56:20 ; Search time 154.902 Seconds  
(without alignments)  
1324.090 Million cells updates/sec

Title: US-10-035-833a-7071  
Perfect score: 40  
Sequence: 1 agctctggagatttttgcagtaagaactaaagggc 40

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications NA.\*  
1: /cgn2\_6/prodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/prodata/2/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/prodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/prodata/2/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/prodata/2/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/prodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
19: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
20: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
21: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	40	16	US-10-035-833a-1246
2	40	100.0	40	16	US-10-035-833a-7071
3	40	100.0	301	9	US-08-783-590-8781
4	40	100.0	2181	10	US-09-999-686-10
5	40	100.0	3118	10	US-09-999-686-19
6	40	100.0	3785	9	US-09-925-302-44
7	40	100.0	3785	9	US-09-925-302-44
8	40	100.0	5102	9	US-09-919-497-8
9	40	100.0	5102	9	US-09-954-531-153
10	40	100.0	5102	10	US-09-960-706-938
11	40	100.0	5102	10	US-09-873-319-615
12	40	100.0	5102	15	US-10-204-752-36
13	40	100.0	5102	15	US-10-641-643-1426
14	40	100.0	5102	17	US-10-775-149-230
15	40	100.0	5128	15	US-10-177-229-96
16	40	100.0	5128	15	US-10-170-385-158
17	40	100.0	5128	15	US-10-170-385-158
18	40	100.0	5128	15	US-10-170-385-158
19	40	100.0	5128	15	US-10-172-118-433
20	40	100.0	5134	10	US-10-342-887-433
21	40	100.0	5134	10	US-09-999-686-11
22	37	92.5	307	16	US-10-242-538A-53750
23	37	92.5	307	16	US-10-083-783A-53750
24	29	72.5	41	16	US-10-035-833A-1245
25	29	72.5	41	16	US-10-035-833A-7070
26	28.8	72.0	174	9	US-09-783-590-8496
27	28.8	72.0	192	9	US-09-783-590-8494
28	24.4	61.0	2129	9	US-09-822-830A-443
29	24	60.0	8349	15	US-10-311-455-1761
30	23.6	59.0	9464	9	US-09-738-847-1
31	23.6	59.0	9464	16	US-10-672-489-1
32	23.6	59.0	9464	16	US-10-673-023-1
33	23.6	59.0	9464	16	US-10-702-755-1
34	23.6	59.0	9464	17	US-10-673-008-1
35	23.2	58.0	507	16	US-10-424-599-126191
36	23	57.5	6191	15	US-10-311-455-1583
37	22.4	56.0	2001	13	US-10-027-632-100363
38	22.4	56.0	2001	13	US-10-027-632-100363
39	22.4	56.0	2008	13	US-10-027-632-97455
40	22.4	56.0	2008	15	US-10-027-632-97455
41	22.4	56.0	17703	16	US-10-257-166-34
42	22	55.0	550	16	US-10-621-901-2167
43	22	55.0	736	16	US-10-424-599-38471
44	22	55.0	4831	15	US-10-172-118-1509
45	22	55.0	4831	16	US-10-342-887-1509
46	21.8	54.5	679	13	US-10-027-632-302658
47	21.8	54.5	679	15	US-10-027-632-302658
48	21.8	54.5	6151	15	US-10-311-455-1583
49	21.6	54.0	539	13	US-10-027-632-50483
50	21.6	54.0	539	13	US-10-027-632-61058
51	21.6	54.0	539	13	US-10-027-632-309745
52	21.6	54.0	539	15	US-10-027-632-61058
53	21.6	54.0	539	15	US-10-027-632-61058
54	21.6	54.0	539	15	US-10-027-632-309745
55	21.6	54.0	539	15	US-10-027-632-309745
56	21.6	54.0	547	13	US-10-027-632-4962
57	21.6	54.0	547	15	US-10-027-632-4962
58	21.6	54.0	595	17	US-10-021-323-15564
59	21.6	54.0	1853	16	US-10-424-599-75043
60	21.6	54.0	9660	11	US-09-997-722-85
61	21.6	54.0	6882	13	US-10-027-632-247490
62	21.4	53.5	6882	13	US-10-027-632-247491
63	21.4	53.5	6882	15	US-10-027-632-247490
64	21.4	53.5	682	15	US-10-027-632-247491
65	21.4	53.5	6215	15	US-10-311-455-99
66	21.4	53.5	6215	15	US-10-311-455-99
67	21.4	53.5	8440	15	US-10-339-676-128
68	21.4	53.5	367378	15	US-10-240-453-220
69	21.4	53.5	329	13	US-10-312-841-1
70	21.2	53.0	529	13	US-10-027-632-248609
71	21.2	53.0	529	13	US-10-027-632-248610
72	21.2	53.0	529	15	US-10-027-632-248610
73	21.2	53.0	573	10	US-09-814-353-4456
74	21.2	53.0	573	10	US-09-814-353-10759
75	21.2	53.0	622	13	US-10-027-632-223889
76	21.2	53.0	622	13	US-10-027-632-223889
77	21.2	53.0	692	10	US-09-814-353-17493
78	21.2	53.0	1091	13	US-10-027-632-259998
79	21.2	53.0	1091	15	US-10-027-632-259998
80	21.2	53.0	1547	10	US-09-814-353-19206
81	21.2	53.0	2011	13	US-10-027-632-259045
82	21.2	53.0	2011	13	US-10-027-632-259045
83	21.2	53.0	2011	13	US-10-027-632-259046
84	21.2	53.0	2011	15	US-10-027-632-259046
85	21.2	53.0	2011	15	US-10-027-632-259045
86	21.2	53.0	2011	15	US-10-027-632-259045
87	21.2	53.0	2011	15	US-10-027-632-259045
88	21.2	53.0	2011	15	US-10-027-632-259045
89	21.2	53.0	2011	15	US-10-027-632-259045
90	21.2	53.0	2011	15	US-10-027-632-259045
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96	21.2	53.0	2011	15	US-10-027-632-259045
97	21.2	53.0	2011	15	US-10-027-632-259045
98	21.2	53.0	2011	15	US-10-027-632-259045
99	21.2	53.0	2011	15	US-10-027-632-259045
100	21.2	53.0	2011	15	US-10-027-632-259045

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:13:20 ; Search time 36.2745 Seconds.  
(without alignments)  
783.789 Million cell updates/sec

Title: US-10-035-833A-7071  
Perfect score: 40  
Sequence: 1 agctctgggagattttttgagtcgaagactaaagggc 40

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: Issued Patents\_NA:\*  
2: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/PCRTUS\_COMB.seq:\*  
7: /cgn2\_6/prodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Length	ID	Description
1	40	100.0	US-09-023-655-1426	Sequence 1426, Ap
2	40	100.0	US-09-919-497-8	Sequence 8, Appl
3	23.6	59.0	US-09-583-580B-1	Sequence 1, Appl
4	23.6	59.0	US-09-738-847-1	Sequence 1, Appl
5	23.6	59.0	US-09-378-810-1	Sequence 679, App
6	21	52.5	US-09-543-681A-679	Sequence 1, Appl
7	21	52.5	US-09-047-026A-1	Sequence 3, Appl
8	20.8	52.0	US-08-475-891A-3	Sequence 31526, A
9	20.6	51.5	US-08-270-767-31526	Sequence 2269, Ap
10	20.6	51.5	US-08-134-001C-2269	Sequence 175, App
11	20.6	51.5	US-08-956-171E-175	Sequence 175, App
12	20.6	51.5	US-08-781-986A-175	Sequence 2813, Ap
13	20.4	51.0	US-09-621-976-2813	Sequence 1, Appl
14	20.4	51.0	US-09-198-452A-1	Sequence 13437, A
15	20.4	51.0	US-09-621-976-13437	Sequence 10381, A
16	20.2	50.5	US-09-270-767-10381	Sequence 2905, Ap
17	20.2	50.5	US-09-107-532A-2905	Sequence 32, Appl
18	20.2	50.5	US-09-288-143-32	Sequence 1244, A
19	20	50.0	US-09-270-767-12442	Sequence 11078, A
20	20	50.0	US-09-171-482-1	Sequence 14296, A
21	20	50.0	US-09-621-976-11078	Sequence 11078, A
22	19.8	49.5	US-09-621-976-11078	Sequence 12146, A
23	19.8	49.5	US-09-513-999C-12146	Sequence 2194, Ap
24	19.8	49.5	US-09-513-999C-12146	Sequence 1, Appl
25	19.8	49.5	US-10-118-328-1	Sequence 17, Appl
26	19.8	49.5	US-09-808-701A-17	Sequence 16, Appl
27	19.8	49.5	US-09-808-701A-17	Sequence 3, Appl
28	19.8	49.5	US-09-808-701A-16	Sequence 3, Appl
29	19.8	49.5	US-10-118-328-3	Sequence 360, Appl
30	19.6	49.0	PCT-US95-08296-23	Sequence 455, App
31	19.6	49.0	US-08-998-416-360	Sequence 455, App
32	19.6	49.0	US-09-641-638-455	Sequence 455, App
33	19.6	49.0	US-10-170-097-455	Sequence 598, App
34	19.6	49.0	US-08-956-171E-558	Sequence 69, Appl
35	19.6	49.0	US-08-781-986A-558	Sequence 77, Appl
36	19.6	49.0	US-08-235-836C-69	Sequence 73, Appl
37	19.6	49.0	US-08-235-836C-77	Sequence 453, Ap
38	19.6	49.0	US-09-540-235-1691	Sequence 71, Appl
39	19.6	49.0	US-08-235-836C-73	Sequence 40, Appl
40	19.6	49.0	US-09-489-039A-4533	Sequence 63, Appl
41	19.6	49.0	US-08-961-527-71	Sequence 2, Appl
42	19.6	49.0	US-08-920-004-3	Sequence 21245, A
43	19.6	49.0	US-09-596-002-40	Sequence 5439, Ap
44	19.6	49.0	US-10-071-411A-63	Sequence 5511, Ap
45	19.6	49.0	US-09-071-411A-63	Sequence 23, Appl
46	19.6	49.0	US-09-513-999C-21245	Sequence 11930, A
47	19.4	48.5	US-09-118-442-23	Sequence 1201, Ap
48	19.4	48.5	US-09-710-879-1201	Sequence 277, App
49	19.4	48.5	US-09-134-001C-277	Sequence 3441, Ap
50	19.4	48.5	US-09-443-681A-3511	Sequence 1, Appl
51	19.4	48.5	US-09-118-442-23	Sequence 25, Appl
52	19.4	48.5	US-08-935-450-1	Sequence 1, Appl
53	19.4	48.5	US-09-166-350-25	Sequence 8, Appl
54	19.4	48.5	US-09-328-123-1	Sequence 10680, A
55	19.4	48.5	US-09-544-398B-8	Sequence 1, Appl
56	19.4	48.5	US-09-543-771-8	Sequence 8, Appl
57	19.4	48.5	US-09-426-90-1	Sequence 18019, A
58	19.4	48.5	US-09-513-999C-18019	Sequence 18944, A
59	19.4	48.5	US-09-513-999C-18944	Sequence 17483, A
60	19.4	48.5	US-09-513-999C-17483	Sequence 1439, A
61	19.2	48.0	US-09-621-976-13479	Sequence 28419, A
62	19.2	48.0	US-08-513-999C-28419	Sequence 42, Appl
63	19.2	48.0	US-10-204-708-42	Sequence 207, App
64	19.2	48.0	US-08-781-981-207	Sequence 207, App
65	19.2	48.0	US-09-618-166-207	Sequence 3, Appl
66	19.2	48.0	US-09-801-876B-3	Sequence 3, Appl
67	19.2	48.0	US-10-254-869-3	Sequence 1, Appl
68	19.2	48.0	US-08-545-528D-1	Sequence 1555, A
69	19.2	48.0	US-09-513-999C-33861	Sequence 16580, A
70	19.2	48.0	US-10-204-708-42	Sequence 10680, A
71	19.2	48.0	US-09-621-976-1555	Sequence 3, Appl
72	19.2	48.0	US-09-270-767-10680	Sequence 3, Appl
73	19.2	48.0	US-09-020-666-3	Sequence 2, Appl
74	19.2	48.0	US-09-192-659-3	Sequence 75, Appl
75	19.2	48.0	US-08-766-551-2	Sequence 60, Appl
76	19.2	48.0	US-08-016-434-76	Sequence 2617, Ap
77	19.2	48.0	US-08-509-712B-60	Sequence 3, Appl
78	19.2	48.0	US-09-543-681A-2617	Sequence 15, Appl
79	19.2	48.0	US-09-813-872-3	Sequence 1, Appl
80	19.2	48.0	US-09-214-139B-3	Sequence 1, Appl
81	19.2	48.0	US-07-906-871-15	Sequence 1, Appl
82	19.2	48.0	US-07-906-871-15	Sequence 1, Appl
83	19.2	48.0	US-09-790-986-1	Sequence 1, Appl
84	19.2	48.0	US-08-916-421A-1	Sequence 1, Appl
85	19.2	48.0	US-09-692-570-1	Sequence 3864, A
86	19.2	48.0	US-09-513-999C-34664	Sequence 3690, Ap
87	19.2	48.0	US-09-513-999C-3690	Sequence 28524, A
88	19.2	48.0	US-09-513-999C-28524	Sequence 32, Appl
89	19.2	48.0	US-08-951-648-32	Sequence 32, Appl
90	19.2	48.0	US-09-177-437-32	Sequence 9069, Ap
91	19.2	48.0	US-09-686-055A-32	Sequence 28247, A
92	19.2	48.0	US-09-621-976-3069	Sequence 6436, Ap
93	19.2	48.0	US-09-270-767-55247	Sequence 21718, A
94	19.2	48.0	US-09-270-767-55247	Sequence 1514, Ap
95	19.2	48.0	US-09-547-681A-1514	Sequence 9942, Ap
96	19.2	48.0	US-09-547-681A-1514	
97	19.2	48.0	US-09-547-681A-1514	
98	19.2	48.0	US-09-547-681A-1514	
99	19.2	48.0	US-09-547-681A-1514	
100	19.2	48.0	US-09-547-681A-1514	

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:35:05 (Search time 172.941 Seconds  
1214.152 Million cell updates/sec

Title: US-10-035-833a-7071  
Perfect score: 40  
Sequence: 1 agctcttgagagattttttgagcgaagactaaaggc 40

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4134866 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database: N\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001as:\*
- 5: Geneseq2001bs:\*
- 6: Geneseq2002as:\*
- 7: Geneseq2002bs:\*
- 8: Geneseq2003as:\*
- 9: Geneseq2003bs:\*
- 10: Geneseq2003cs:\*
- 11: Geneseq2003ds:\*
- 12: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	40	100.0	40	6	ABZ44462 Human cyt
2	40	100.0	40	6	ABZ50289 Human cyt
3	40	100.0	3785	3	AAFI8025 Lung can
4	40	100.0	5102	6	ABO79929 Human CYP
5	40	100.0	5102	6	ABK35488 Human end
6	40	100.0	5102	6	ABK62883 Breast ca
7	40	100.0	5102	6	ABK64720 Human ben
8	40	100.0	5102	6	AAI39861 Human all
9	40	100.0	5102	10	ADD14611 Human src
10	40	100.0	5102	10	ACC46768 Human COP
11	40	100.0	5102	11	AD132100 Human CDN
12	40	100.0	5128	6	ABV78036 Hypoxia-r
13	40	100.0	5128	6	ABV77942 Hypoxia-l
14	40	100.0	5128	8	ACFC3492 Gene enco
15	40	100.0	5128	8	ACCS0124 Breast ca
16	40	100.0	5128	12	ADN03862 Antipsoi
17	40	100.0	5134	6	ABK88882 Human CYP
18	40	100.0	10254	6	ABN81206 Human CYP
19	29	72.5	41	6	ABZ44461 Human cyt
20	29	72.5	41	6	ABZ50288 Human cyt
21	29	72.5	5329	6	AA594902 Human DNA

22	24.4	61.0	2169	6	AA62656	AA62656 CDNA sequ
23	24	60.0	251	2	AAI11003	AAI11003 Human bla
24	24	60.0	350	2	AAH87238	AAH87238 Human sin
25	24	60.0	8349	6	AB133788	AB133788 Human imm
26	23.8	59.5	11000	2	AAZ01425_07	Continuation (8 of
27	23.6	59.0	9464	4	AAE6944	AAE6944 Nucleotid
28	23.6	59.0	9467	4	AAZ99678	AAZ99678 DNA sequ
29	23	57.5	6191	6	ABL33370	ABL33370 Human imm
30	22.6	56.5	101	10	ADB75927	ADB75927 Tomato pl
31	22.6	56.5	2263	4	ABL04390	ABL04390 Drosophi
32	22.4	56.0	17703	6	ABK39953	ABK39953 Human che
33	22	55.0	350	12	AD111725	AD111725 Cat filea
34	22	55.0	744	10	ACF68467	ACF68467 Photorhab
35	22	55.0	4129	12	ADU72016	ADU72016 Human PMW
36	22	55.0	10264	10	ACF65378	ACF65378 Photorhab
37	22	55.0	110000	10	ACF67367_11	Continuation (12 o
38	22	55.0	110000	10	ACF67367_12	Continuation (13 o
39	21.8	54.5	597	5	ABV55315	ABV55315 Human pro
40	21.8	54.5	2000	8	ADA72356	ADA72356 Rice gene
41	21.8	54.5	6151	6	ABL33610	ABL33610 Human imm
42	21.8	54.5	6151	6	ABK28275	ABK28275 DNA trans
43	21.6	54.0	569	4	AAH10768	AAH10768 Human CDN
44	21.6	54.0	1833	4	AAH15049	AAH15049 Human CDN
45	21.6	54.0	3752	6	ABK13001	ABK13001 DNA encod
46	21.6	54.0	12301	5	AAK34544	AAK34544 Human DNA
47	21.6	54.0	96599	10	ADC85298	ADC85298 Human Bgr
48	21.6	54.0	96600	9	ADA02819	ADA02819 Mouse Sbs
49	21.6	54.0	96600	10	ADB72557	ADB72557 Mouse Sbs
50	21.6	54.0	96600	12	ADM74414	ADM74414 Murine ca
51	21.4	53.5	393	2	AAO59549	AAO59549 Human bra
52	21.4	53.5	6215	6	ABL32126	ABL32126 Human imm
53	21.4	53.5	6215	6	ABN79998	ABN79998 Human che
54	21.4	53.5	6282	4	AAH45421	AAH45421 Chemically
55	21.4	53.5	7537	4	ABL09602	ABL09602 Drosophila
56	21.4	53.5	8440	6	ABK28346	ABK28346 DNA trans
57	21.4	53.5	15430	4	AAK70953	AAK70953 Human imm
58	21.4	53.5	110000	10	ADH10017_1	Continuation (2 of
59	21.2	53.0	363	2	AAT22619	AAT22619 Human gen
60	21.2	53.0	373	5	AAI66690	AAI66690 Human pol
61	21.2	53.0	373	5	ADL36869	ADL36869 Human ova
62	21.2	53.0	573	5	ADL36869	ADL36869 Human ova
63	21.2	53.0	573	5	ADL36869	ADL36869 Human ova
64	21.2	53.0	1547	5	ADL45316	ADL45316 Human ova
65	21.2	53.0	5722	6	ABK31441	ABK31441 Signal tr
66	21.2	53.0	5722	6	ABL70416	ABL70416 Chemically
67	21.2	53.0	5722	6	ABK63359	ABK63359 Human gen
68	21.2	53.0	100267	6	ABT11032	ABT11032 Human die
69	21.2	52.5	427	8	ABX43206	ABX43206 Bovine ES
70	21	52.5	480	3	AAK53860	AAK53860 Arabidops
71	21	52.5	589	3	AAK53860	AAK53860 Arabidops
72	21	52.5	1040	6	ABO76438	ABO76438 S. cerevi
73	21	52.5	1083	10	ADP00394	ADP00394 Bacterial
74	21	52.5	1565	3	AAK37656	AAK37656 Arabidops
75	21	52.5	1565	3	AAK37656	AAK37656 Arabidops
76	21	52.5	2154	12	ADK67445	ADK67445 Baker's y
77	21	52.5	4125	3	AAK50716	AAK50716 Arabidops
78	21	52.5	4906	3	AAZ45133	AAZ45133 Saccharom
79	21	52.5	28564	10	ADD48770	ADD48770 Human gen
80	21	52.5	53585	2	AAK20251	AAK20251 Borrelia
81	21	52.5	93000	12	ADQ79405	ADQ79405 CENPc re
82	21	52.5	110000	2	AAK20248_04	Continuation (5 of
83	21	52.5	116277	2	AAK20248	AAK20248 Borrelia
84	21	52.5	210204	10	ADL13752	ADL13752 Osteoarth
85	20.8	52.0	366	4	AAI39108	AAI39108 Human pol
86	20.8	52.0	431	10	ABV80704	ABV80704 Leukaemia
87	20.8	52.0	435	5	ABV52027	ABV52027 Human pro
88	20.8	52.0	679	3	AAK44003	AAK44003 Arabidops
89	20.8	52.0	829	3	AAK51899	AAK51899 Human col
90	20.8	52.0	2183	4	AAK51899	AAK51899 Human col
91	20.8	52.0	4897	12	ADU12544	ADU12544 DNA fragm
92	20.8	52.0	4908	10	ADF82102	ADF82102 Leukaemia
93	20.8	52.0	4908	10	ADF82101	ADF82101 Leukaemia
94	20.8	52.0	4908	10	ADF82100	ADF82100 Leukaemia

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CM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:40:10 ; Search time 702.549 Seconds

(without alignments)  
2692.464 Million cell updates/sec

Title: US-10-035-833a-7071

Perfect score: 40  
Sequence: 1 agctctggagagatttttttgagtcagaagacttaagggc 40

Scoring table: IDENTITY NUC  
Gapop 1.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

Database :

Genbm1: \*  
1: gb\_ba: \*  
2: gb\_atg: \*  
3: gb\_in: \*  
4: gb\_ov: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_dr: \*  
10: gb\_ro: \*  
11: gb\_ste: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	40	6	AX515048
2	40	100.0	40	6	AX515048 Sequence
3	40	100.0	2181	6	AX520873
4	40	100.0	2799	6	AX566080
5	40	100.0	3118	6	BC012049
6	40	100.0	3124	11	G06772
7	40	100.0	5102	6	BD176699
8	40	100.0	5102	6	AR380881
9	40	100.0	5102	6	AX330711
10	40	100.0	5102	6	AX563644
11	40	100.0	5102	6	BD169898
12	40	100.0	5102	6	HSU03688
13	40	100.0	5104	6	CO714214
14	40	100.0	5134	6	AX666071
15	40	100.0	5234	11	BV177879
16	40	100.0	12177	9	HSU56438
17	40	100.0	79303	2	AC011074
18	40	100.0	209156	2	AC009229
19	40	100.0	211222	2	AC022097

20	37	92.5	307	6	C0708824	C0708824 Sequence
21	29	72.5	41	6	AX515047	AX515047 Sequence
22	29	72.5	41	6	AX520872	AX520872 Sequence
23	29	72.5	1596	6	AF450130S	AF450130S Homo sapi
24	29	72.5	5329	6	AX281748	AX281748 Sequence
25	29	72.5	12124	2	AX393998	AX393998 Homo sapi
26	26.2	65.5	84742	2	AC099937	AC099937 Mus muscu
27	25	62.5	180835	2	BX957237	BX957237 Danio rer
28	24.2	60.5	165964	2	AC128313	AC128313 Rattus no
29	24.2	60.5	195545	2	AC121701	AC121701 Rattus no
30	24.2	60.5	214363	2	AC109876	AC109876 Rattus no
31	24.2	60.5	234450	2	AC132162	AC132162 Rattus no
32	24.2	60.5	237462	2	AC097120	AC097120 Rattus no
33	24	60.0	8349	6	AX346690	AX346690 Sequence
34	24	60.0	163399	2	AL671920	AL671920 Mouse DNA
35	24	60.0	203953	10	AC087560	AC087560 Mus muscu
36	24	60.0	228059	2	AC109886	AC109886 Rattus no
37	24	60.0	275742	2	AC096514	AC096514 Rattus no
38	23.8	59.5	12088	1	AE001334	AE001334 Chlamydia
39	23.8	59.5	128965	2	AL357562	AL357562 Human DNA
40	23.8	59.5	146275	2	AC080119	AC080119 Homo sapi
41	23.8	59.5	150026	2	AL589868	AL589868 Homo sapi
42	23.8	59.5	199894	2	AC149799	AC149799 Aedes aeg
43	23.8	59.5	234795	2	AL391236	AL391236 Homo sapi
44	23.8	59.5	236203	2	AC096613	AC096613 Rattus no
45	23.8	59.5	335695	2	AC111623	AC111623 Rattus no
46	23.6	59.0	4373	10	BC076615	BC076615 Mus muscu
47	23.6	59.0	6345	10	D83033	D83033 Mouse mRNA
48	23.6	59.0	9464	6	E43300	E43300 Composition
49	23.6	59.0	9464	6	AR441877	AR441877 Sequence
50	23.6	59.0	9464	6	AR490814	AR490814 Sequence
51	23.6	59.0	9464	6	AX135034	AX135034 Sequence
52	23.6	59.0	32679	3	CE120D3	CE120D3 Caenorhabdi
53	23.6	59.0	158861	10	AL845273	AL845273 Mouse DNA
54	23.6	59.0	163640	2	AC093328	AC093328 Homo sapi
55	23.6	59.0	167794	2	AF215844	AF215844 Homo sapi
56	23.6	59.0	167710	9	AL591463	AL591463 Human DNA
57	23.6	59.0	226460	10	AC098730	AC098730 Mus muscu
58	23.6	59.0	223041	2	AC113842	AC113842 Rattus no
59	23.6	59.0	257396	2	AC095924	AC095924 Rattus no
60	23.6	59.0	269912	2	AC094291	AC094291 Rattus no
61	23.2	58.0	826	8	AF124833	AF124833 Malus dom
62	23.2	58.0	87967	8	AC005223	AC005223 Arabidops
63	23.2	58.0	137749	2	AC109361	AC109361 Homo sapi
64	23.2	58.0	181401	2	AL954127	AL954127 Mus muscu
65	23.2	58.0	186547	10	AL772156	AL772156 Mouse DNA
66	23.2	58.0	189876	9	AL357892	AL357892 Human DNA
67	23.2	58.0	227477	2	AC097083	AC097083 Rattus no
68	23.2	58.0	248510	2	AC095814	AC095814 Rattus no
69	23.2	58.0	254381	2	AC128334	AC128334 Rattus no
70	23.2	58.0	285107	2	AC103104	AC103104 Rattus no
71	23	57.5	6191	5	CR389425	CR389425 Gallus ga
72	23	57.5	25305	3	CE735C8	CE735C8 Caenorhabdi
73	23	57.5	79284	2	EX927314	EX927314 Danio rer
74	23	57.5	155255	9	AL359238	AL359238 Human chr
75	23	57.5	166870	9	HSBA425M5	HSBA425M5 Human chr
76	23	57.5	194433	9	AP006571	AP006571 Gloeobact
77	23	57.5	299700	1	G61210	G61210 SHGC-85518
78	22.8	57.0	517	11	AC149156	AC149156 Xenopus t
79	22.8	57.0	70095	2	AC022587	AC022587 Homo sapi
80	22.8	57.0	73227	2	AL662788	AL662788 Human DNA
81	22.8	57.0	106363	9	AE014177_2	AE014177_2 Cont. of
82	22.8	57.0	110000	10	AC103851	AC103851 Homo sapi
83	22.8	57.0	111762	9	HSJ18113	HSJ18113 Human DNA
84	22.8	57.0	118271	9	AL96867	AL96867 Mouse DNA
85	22.8	57.0	121094	10	AC074081	AC074081 Homo sapi
86	22.8	57.0	125147	2	AC122058	AC122058 Mus muscu
87	22.8	57.0	149331	10	AC02181	AC02181 Homo sapi
88	22.8	57.0	149109	2	AC06580	AC06580 Homo sapi
89	22.8	57.0	149252	2	AL512350	AL512350 Homo sapi
90	22.8	57.0	150180	2	CR392342	CR392342 Danio rer
91	22.8	57.0	150180	2	CR392342	CR392342 Danio rer
92	22.8	57.0	150180	2	CR392342	CR392342 Danio rer



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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:11:10 ; Search time 1452.89 Seconds  
(without alignments)  
1028.317 Million cell updates/sec

Title: US-10-035-833a-7064

Perfect score: 41  
Sequence: 1 tgcagcagctaccaccta.....ttcctctgattttgagfca 41

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

Database :

EST: \*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.6	99.0	775	8	AQ740902 HS.2274.A
2	25.8	62.9	832	2	BP667994 60328773
3	24.6	60.0	545	5	BM961466 C1A1K207
4	24.2	59.0	377	8	AZ046892 nbeD0088L
5	24.2	59.0	753	9	CL610449 OR_BBA000
6	23.6	57.6	758	9	CR239831 Reverse s
7	23.6	57.6	262	2	BB718435 BB718435
8	23.6	57.6	379	5	BQ703520 EST68.alm
9	23.6	57.6	560	2	AM642665 cm21c01.w
10	23.6	57.6	599	2	AM329910 TENU4717
11	23.6	57.6	638	9	AG017891 Homo sapi
12	23.6	57.6	645	9	AG017885 Homo sapi
13	23.6	57.6	742	5	BU219688 603750155
14	23.6	57.6	964	9	CNS019688 Tetradon
15	23.4	57.1	430	8	AZ035357 PRC1-23-2
16	23.4	57.1	782	7	CK359869 AGENCOURT
17	23.2	56.6	215	6	CD946458 REX99.9e
18	23.2	56.6	409	2	BB607500
19	23.2	56.1	429	2	AW934665
20	23.2	56.1	502	4	BG551297 ead35G04.
21	23.2	56.1	517	2	BE449596 EST356355
22	23.2	56.1	534	8	B2837488 CH240.248
23	23.2	56.1	569	5	B0094749 sam51001
24	23.2	56.1	614	5	BU926165 sas87c06.





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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:35:05 ; Search time 177.265 seconds  
(without alignments)  
1214.152 Million cell updates/sec

Title: US-10-035-833a-7064  
Perfect score: 41  
Sequence: 1 tgcacgacactcaccaccta.....ttccctctgatttgcgtca 41

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

N\_Geneseq\_23Sep04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40.6	99.0	41	6	ABZ50282 Human cyf
2	40.6	99.0	41	6	ABZ44455 Human cyf
3	31.4	76.6	5735	6	ABK40066 Human che
4	23	56.1	5735	6	ABK40065 Human che
5	22.2	54.1	470	6	AAS31566 Human pol
6	22.2	54.1	470	6	ABQ66890 Human dna
7	22.2	54.1	470	10	ADCI1177 Human dna
8	21.6	53.2	9046	4	AAK87480 Human imm
9	21.6	52.7	721	4	AAI94863 Human neu
10	21.6	52.7	873	4	AAH07369 Human cdn
11	21.6	52.7	1728	4	AAH14783 Human cdn
12	21.6	52.7	2733	3	AAZ57852 Protein r
13	21.6	52.7	2775	5	AAS80660 DNA encod
14	21.6	52.7	4237	10	ADP82127 Leukemia
15	21.2	51.7	567	4	AAK92572 Human cdn
16	21.2	51.7	567	4	AAK94075 Human cdn
17	21.2	51.7	567	12	ADL28999 3' end of
18	21.2	51.7	567	12	ADL30502 3' end of
19	21.2	51.7	1488	4	ABL15559 Drosophi
20	21.2	51.7	4003	4	ABL15558 Drosophi
21	21.2	51.7	80374	12	ADM88956 Diterpene

22	51.2	1278	10	ACF70673	Act70673 Phototax
23	51.2	32404	9	ADA02894	Ada02894 Human BLR
24	51.2	32404	10	ADB72632	ADB72632 Human BLR
25	51.2	32404	10	ADC85373	ADC85373 Mouse BLR
26	51.2	32404	12	ADM74489	ADM74489 Human car
27	51.2	110000	10	ACF67367	Continuation (38 o
28	51.2	110000	10	ACF65388	Continuation (11 o
29	50.7	587	2	AAV42942	AAV42942 Streptoco
30	50.7	1731	6	AAV57025	AAV57025 C. pneumo
31	50.7	1731	6	ABL92668	ABL92668 Chlamydia
32	50.7	1731	10	ADP42819	ADP42819 Chlamydia
33	50.7	6004	2	AAV52160	AAV52160 Streptoco
34	50.7	8499	4	ABL16018	ABL16018 Drosophi
35	50.7	110000	2	AAK19990	AAK19990 Nucleotid
36	50.7	110000	10	ABZ56454	Continuation (5 of
37	50.2	705	10	ADK54621	ADK54621 Plant DNA
38	50.2	831	4	AAK93836	AAK93836 Human cdn
39	50.2	831	4	AAK91673	AAK91673 Human cdn
40	50.2	831	12	ADL30263	ADL30263 3' end of
41	50.2	1192	5	ADM19342	ADM19342 Novel hum
42	50.2	2375	4	AAK94180	AAK94180 Human ful
43	50.2	2375	12	ADL30689	ADL30689 Full leng
44	50.2	2548	5	ADM19592	ADM19592 Novel hum
45	50.2	2548	5	AAK76597	AAK76597 DNA encod
46	50.2	2743	5	ADA52846	ADA52846 Human cod
47	50.2	3849	10	ABL03432	ABL03432 Drosophi
48	50.2	4359	4	ABL19258	ABL19258 Drosophi
49	50.2	17203	4	ABA68567	ABA68567 Human foe
50	50.2	17203	4	ABA35547	ABA35547 Probe #14
51	50.2	17203	4	AAK42707	AAK42707 Human bon
52	50.2	17203	4	AAK42707	AAK42707 Human bon
53	50.2	17203	4	AAK16933	AAK16933 Human bra
54	50.2	17203	4	ABZ42327	ABZ42327 Human liv
55	50.2	17203	5	AAI09088	AAI09088 Probe #90
56	50.2	17203	12	ACH87619	ACH87619 Human gen
57	50.2	81940	4	AAK03390	AAK03390 Human tit
58	50.2	81940	6	ABK64829	ABK64829 Human ben
59	50.2	81940	12	ADQ17315	ADQ17315 Human soc
60	50.2	93801	9	ABX13540	ABX13540 Human RGS
61	50.2	110000	6	ABA90193	ABA90193 Human oes
62	50.2	110000	6	ABQ87681	ABQ87681 Human oes
63	50.2	110000	8	ABX37171	Gene enco
64	49.8	294	2	AAI25304	AAI25304 Human gen
65	49.8	296	2	AAV88071	AAV88071 Est clone
66	49.8	706	3	AAZ98110	AAZ98110 Human sig
67	49.8	734	2	AAK86150	AAK86150 Nucleotid
68	49.8	1677	2	AAQ46589	AAQ46589 Alcohol o
69	49.8	2151	5	ADL62360	ADL62360 Human sec
70	49.8	2500	6	ABZ11364	ABZ11364 Human pol
71	49.8	2500	12	ADM43882	ADM43882 Novel hum
72	49.8	2717	10	ADCI3302	ADCI3302 DNA of Hi
73	49.8	2789	6	ABQ70842	ABQ70842 Listeria
74	49.8	3246	12	ADH56194	ADH56194 Arabidops
75	49.8	3246	12	ADH56192	ADH56192 Arabidops
76	49.8	3718	4	AAK90359	AAK90359 Human dig
77	49.8	3718	4	AAK90360	AAK90360 Human dig
78	49.8	3718	4	AAK73104	AAK73104 Human imm
79	49.8	3718	4	AAK87573	AAK87573 Human imm
80	49.8	3718	4	AAK875120	AAK875120 Human imm
81	49.8	3718	4	AAK87443	AAK87443 Human imm
82	49.8	3718	4	AAK87592	AAK87592 Human imm
83	49.8	3718	4	AAK87442	AAK87442 Human imm
84	49.8	3718	4	AAK87443	AAK87443 Human rep
85	49.8	3718	4	AAK87443	AAK87443 Human rep
86	49.8	3718	4	AAK87443	AAK87443 Human rep
87	49.8	3718	5	AAK87443	AAK87443 Human rep
88	49.8	3718	5	AAK87443	AAK87443 Human rep
89	49.8	3718	5	AAK87443	AAK87443 Human rep
90	49.8	3718	9	ADK13875	ADK13875 Human nov
91	49.8	3718	12	ADN41665	ADN41665 Novel hum
92	49.8	3718	12	ADN41666	ADN41666 Novel hum
93	49.8	200620	12	ADN41666	ADN41666 Novel hum
94	49.3	413	8	ABX62408	ABX62408 Arabidops

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:40:10 ; Search time 720.113 Seconds  
(without alignments)

2692.464 Million cell updates/sec

Title: US-10-035-833a-7064

Perfect score: 41  
Sequence: 1 tgcagcagctaccaccta.....ttccctcgtatttgatca 41

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 segs, 23644843745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seg length: 0  
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl:\*\*  
1: gb\_ba:\*\*  
2: gb\_hcg:\*\*  
3: gb\_in:\*\*  
4: gb\_om:\*\*  
5: gb\_ov:\*\*  
6: gb\_pat:\*\*  
7: gb\_ph:\*\*  
8: gb\_pi:\*\*  
9: gb\_pr:\*\*  
10: gb\_ro:\*\*  
11: gb\_sts:\*\*  
12: gb\_sy:\*\*  
13: gb\_un:\*\*  
14: gb\_yi:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.6	99.0	41	6	AXS15041 Sequence
2	40.6	99.0	41	6	AXS20866 Sequence
3	40.6	99.0	79303	2	AC011074 Homo sapi
4	40.6	99.0	209156	9	AC009329 Homo sapi
5	40.6	99.0	212222	2	AC0022097 Homo sapi
6	31.4	76.6	5735	6	AX348453 Sequence
7	24.6	60.0	229045	9	AC008680 Homo sapi
8	24.6	60.0	236365	2	AC0087099 Mus muscu
9	24.2	59.0	151506	8	OSJN00080 Oryza sat
10	24.2	59.0	156077	9	AL354997 Human DNA
11	24.2	59.0	165745	8	OSJN00105 Oryza sat
12	24.2	59.0	228427	10	AC107738 Mus muscu
13	24.2	58.0	262288	2	AC103137 Rattus no
14	23.8	58.0	263283	2	AC109389 Rattus no
15	23.6	57.6	164221	2	AC148133 Ateleiix
16	23.6	57.6	227579	2	AC150579 Bos tauru
17	23.4	57.1	124518	9	AL138962 Human DNA
18	23.4	57.1	136155	10	AC132586 Mus muscu
19	23.4	57.1	174426	10	AC142504 Mus muscu

20	23.4	57.1	180516	10	AC122442 Mus muscu
21	23.4	57.1	180602	10	AC134429 Mus muscu
22	23.4	57.1	211871	10	AL672306 Mouse DNA
23	23.4	57.1	215319	2	AC099473 Rattus no
24	23.4	57.1	218270	2	AC079499 Mus muscu
25	23.4	57.1	224373	2	AC098129 Rattus no
26	23.4	57.1	240482	2	AC122975 Rattus no
27	23.4	57.1	347664	10	BX883043 Rattus no
28	23.2	56.6	223200	2	AC109959 Rattus no
29	23.2	56.6	249667	2	AC114720 Rattus no
30	23.2	56.6	277490	2	AC097085 Rattus no
31	23	56.1	5735	6	AX348452 Sequence
32	23	56.1	63352	2	AC110047 Homo sapi
33	23	56.1	67822	2	AC027792 Homo sapi
34	23	56.1	129285	5	AC091726 Gallus ga
35	23	56.1	157081	2	AC023084 Homo sapi
36	23	56.1	161842	2	AC107931 Homo sapi
37	23	56.1	162066	9	AC018989 Homo sapi
38	23	56.1	173693	2	AC142422 Rattus no
39	23	56.1	174152	10	AC132133 Mus muscu
40	23	56.1	176643	9	AC005324 Homo sapi
41	23	56.1	197470	2	AC026964 Homo sapi
42	23	56.1	203810	10	AC132612 Mus muscu
43	23	56.1	247189	2	AC109910 Rattus no
44	23	56.1	251589	2	AC111900 Rattus no
45	23	56.1	258648	2	AC130010 Rattus no
46	23	56.1	311823	2	AC095562 Rattus no
47	22.8	55.6	454	11	BV184132 Continuation (5 of
48	22.8	55.6	110000	2	AC107201-4 AC094080 Homo sapi
49	22.8	55.6	118504	9	AC094080 Homo sapi
50	22.8	55.6	133054	10	AC107447 Rattus no
51	22.8	55.6	150528	9	AC010260 Homo sapi
52	22.8	55.6	152838	2	AC011589 Homo sapi
53	22.8	55.6	170797	9	AC011379 Homo sapi
54	22.8	55.6	208764	10	AC098875 Mus muscu
55	22.8	55.6	210675	2	AC026272 Homo sapi
56	22.8	55.6	211034	10	AL731709 Mus muscu
57	22.8	55.6	218170	10	AC102119 Mus muscu
58	22.8	55.6	225342	2	AC132765 Rattus no
59	22.8	55.6	231155	2	AC123664 Mus muscu
60	22.8	55.6	243640	2	AC108571 Rattus no
61	22.8	55.6	256020	2	AC115250 Rattus no
62	22.8	55.6	275059	2	AC120776 Rattus no
63	22.6	55.1	81019	2	AC149536 Xenopus t
64	22.6	55.1	93010	10	AL627386 Mouse DNA
65	22.6	55.1	113715	2	AC149149 Xenopus t
66	22.6	55.1	134666	2	AC146759 Mus muscu
67	22.6	55.1	180485	2	AC027145 Homo sapi
68	22.6	55.1	180725	2	AC119511 Rattus no
69	22.6	55.1	196755	2	AC140779 Mus muscu
70	22.6	55.1	210562	2	AC134489 Rattus no
71	22.6	55.1	227996	2	AC117916 Rattus no
72	22.6	55.1	234859	2	AC128112 Rattus no
73	22.6	55.1	247577	2	AC106830 Rattus no
74	22.6	55.1	261708	2	AC098350 Rattus no
75	22.6	55.1	282849	2	AC132855 Rattus no
76	22.6	54.6	69337	2	AC101261 Mus muscu
77	22.4	54.6	140575	8	AP005502 Oryza sat
78	22.4	54.6	146473	2	AC149883 Xenopus t
79	22.4	54.6	159409	8	AP004634 Oryza sat
80	22.4	54.6	166272	10	AC131794 Mus muscu
81	22.4	54.6	168199	2	AC116042 Papio ham
82	22.4	54.6	168380	2	AC116043 Papio ham
83	22.4	54.6	179454	2	AC123737 Mus muscu
84	22.4	54.6	181442	10	AC114917 Mus muscu
85	22.4	54.6	184634	10	AC115359 Mus muscu
86	22.4	54.6	185027	2	AC123234 Rattus no
87	22.4	54.6	210148	10	AL928791 Mouse DNA
88	22.4	54.6	236247	2	AC123009 Rattus no
89	22.4	54.6	265537	2	AC087228 Mus muscu
90	22.2	54.1	29682	2	AC012638 Homo sapi
91	22.2	54.1	93511	9	BX927732 Human DNA
92	22.2	54.1	102196	9	CR388415 Human DNA

